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Date completed: 06-12-03

Searcher: Beverly 84994

Terminal time: 26

| Search Site | Vendors |
|---|---|
| _____ STIC | _____ IG |
| _____ CM-1 | _____ STN |

FILE 'REGISTRY' ENTERED AT 16:08:38 ON 12 JUN 2003
L1 4786 SEA ABB=ON PLU=ON GCCTCTGGGGAG/SQSN

FILE 'HCAPLUS' ENTERED AT 16:10:15 ON 12 JUN 2003
L2 666 SEA ABB=ON PLU=ON L1
L3 2 SEA ABB=ON PLU=ON L2 AND (B3 OR BETA3 OR BETA 3)(W)(AR OR ADRENERG?)
L4 19 SEA ABB=ON PLU=ON L2 AND TRANSCRIPTION? REGULAT?
L5 19 SEA ABB=ON PLU=ON L3 OR L4

L5 ANSWER 1 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2003:409169 HCAPLUS
TITLE: Genes that are differentially expressed during erythropoiesis and their diagnostic and therapeutic uses
INVENTOR(S): Brissette, William H.; Neote, Kuldeep S.; Zagouras, Panayiotis; Zenke, Martin; Lemke, Britt; Hacker, Christine
PATENT ASSIGNEE(S): Pfizer Products Inc., USA; Max-Delbruck-Centre for Molecular Medicine
SOURCE: PCT Int. Appl., 285 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 2003038130 | A2 | 20030508 | WO 2002-XA34888 | 20021031 |
| W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG | | | | |
| WO 2003038130 | A2 | 20030508 | WO 2002-US34888 | 20021031 |
| W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG | | | | |

PRIORITY APPLN. INFO.:
US 2001-335048P P 20011031
US 2001-335183P P 20011102
WO 2002-US34888 A 20021031

AB The present invention provides mol. targets that regulate erythropoiesis. Groups of genes or their encoded gene products

comprise panels of the invention and may be used in therapeutic intervention, therapeutic agent screening, and in diagnostic methods for diseases and/or disorders of erythropoiesis. The panels were discovered using gene expression profiling of erythroid progenitors with Affymetrix HU6800 and HG-U95Av2 chips. Cells from an in vitro growth and differentiation system of SCF-Epo dependent human erythroid progenitors, E-cadherin+/CD36+ progenitors, cord blood, or CD34+ peripheral blood stem cells were analyzed. The HU6800 chip contains probes from 13,000 genes with a potential role in cell growth, proliferation, and differentiation and the HG-U95Av2 chip contains 12,000 full-length, functionally-characterized genes. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **389189-05-3**, DNA (human clone lambda A3. )
**391788-88-8**, DNA (human clone Qc-9D3 )
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; genes that are differentially expressed during erythropoiesis and their diagnostic and therapeutic uses)

L5 ANSWER 2 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2003:205655 HCAPLUS
DOCUMENT NUMBER: 138:199856
TITLE: Regulation of the pancreatic pro-endocrine gene neurogenin3. [Erratum to document cited in CA136:146041]
AUTHOR(S): Lee, Jane C.; Smith, Stuart B.; Watada, Hirotaka; Lin, Joseph; Scheel, David; Wang, Juehu; Mirmira, Raghavendra G.; German, Michael S.
CORPORATE SOURCE: Hormone Research Institute and the Department of Pediatrics, University of California, San Francisco, CA, 94143, USA
SOURCE: Diabetes (2001), 50(6), 1512
CODEN: DIAEAZ; ISSN: 0012-1797
PUBLISHER: American Diabetes Association
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The correct spelling of Dr. Smith's name is Stuart B. Smith.
IT **390513-25-4**, GenBank AF234829
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; regulation of pancreatic pro-endocrine neurogenin3 gene in human and mouse (Erratum))

L5 ANSWER 3 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2003:187090 HCAPLUS
DOCUMENT NUMBER: 138:219712
TITLE: Differentially expressed gene expression profiles in human glomerular diseases
INVENTOR(S): Munger, William E.; Falk, Ronald; Sun, Hongwei; Sasai, Hitoshi; Waga, Iwao; Yamamoto, Jun
PATENT ASSIGNEE(S): Gene Logic, Inc., USA; University of North Carolina At Chapel Hill
SOURCE: PCT Int. Appl., 781 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 9
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 2003016476 | A2 | 20030227 | WO 2002-XG25766 | 20020814 |
| W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG | | | | |
| WO 2003016476 | A2 | 20030227 | WO 2002-US25766 | 20020814 |
| WO 2003016476 | A3 | 20030508 | | |
| W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG | | | | |

PRIORITY APPLN. INFO.: US 2001-311837P P 20010814
WO 2002-US25766 A 20020814

AB The present invention is based on the elucidation of global changes in gene expression in peripheral blood leukocytes (PBL) of patients with glomerular diseases exhibiting different types of clin. and pathol. features of glomerular nephropathy as compared to normal PBL as well as the identification of individual genes that are differently expressed in PBL of patients with glomerular diseases. The genes and gene expression information may be used as markers for the diagnosis of disease subtype, such as IgA nephropathy, Minimal Change nephrotic syndrome, antineutrophil cytoplasmic antibody-assocd. glomerulonephritis (ANCA), focal segmental glomerulosclerosis (FSGS), and lupus nephritis. The genes may also be used as markers to evaluate the effects of a candidate drug or agent on tissues, including PBLs, particularly PBLs undergoing activation or PBLs from a patient with glomerular disease. Differential expression of genes between PBLs from patients with glomerular disease and normal PBL samples was detd. using the Affymetrix 42K human gene chip set. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L5 ANSWER 4 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:696159 HCAPLUS
DOCUMENT NUMBER: 137:246071
TITLE: Gene expression profiles relating to normal and

osteoarthritic cartilage
INVENTOR(S): Liew, Choong-Chin; Marshall, Wayne E.; Zhang, Hongwei
PATENT ASSIGNEE(S): Chondrogene Inc., Can.
SOURCE: PCT Int. Appl., 777 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 2002070737 | A2 | 20020912 | WO 2002-CA247 | 20020228 |
| WO 2002070737 | C1 | 20021031 | | |

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2001-271955P P 20010228
US 2001-275017P P 20010312
US 2001-305340P P 20010713

AB The invention provides gene expression profiles comprising one or more polynucleotide sequences that are expressed in chondrocytes from any of the following developmental and disease stages: fetus, normal adult, mild osteoarthritis, moderate osteoarthritis, marked osteoarthritis, and severe osteoarthritis. Complementary DNA libraries were constructed from human fetal, normal, mild osteoarthritic and severe osteoarthritic cartilage samples (13,398, 17,151, 12,651, and 14,222 expressed sequence tags (ESTs), resp.). The known and novel clones derived from these libraries were then used to construct human chondrocyte-specific microarrays to generate differential gene expression profiles useful as a diagnostic tools for detection of osteoarthritis. A total of 5807 expressed gene sequences are provided and matched to known gene sequences, other ESTs, or mitochondrial, ribosomal, vector, and cDNA/hypothetical protein sequences in the public databases. Arrays of the invention are useful as a gold std. for osteoarthritis diagnosis and for use to identify and monitor therapeutic efficacy of new drug targets.

IT **227594-62-9**, DNA (human gene KvLQT1 plus gene KvLQT1)
**258491-28-0 266660-95-1 267626-85-7**, DNA (human gene GLP plus flanks) **385252-57-3 392013-60-4**, GenBank AC002400
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; gene expression profiles relating to normal and osteoarthritic cartilage)

L5 ANSWER 5 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:611070 HCAPLUS
Correction of: 2002:158040

DOCUMENT NUMBER: 137:120745
Correction of: 136:195361
TITLE: Stress-regulated genes of Arabidopsis thaliana and generation and uses of transgenic plants containing them
INVENTOR(S): Harper, Jeffrey F.; Kreps, Joel; Wang, Xun; Zhu, Tong
PATENT ASSIGNEE(S): The Scripps Research Institute, USA; Syngenta Participations A.-G.
SOURCE: PCT Int. Appl., 577 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 2002016655 | A2 | 20020228 | WO 2001-US26685 | 20010824 |
| WO 2002016655 | C2 | 20030109 | | |
| WO 2002016655 | A3 | 20030313 | | |
| W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG | | | | |
| AU 2001086811 | A5 | 20020304 | AU 2001-86811 | 20010824 |
| US 2002160378 | A1 | 20021031 | US 2001-938842 | 20010824 |
| EP 1313867 | A2 | 20030528 | EP 2001-966283 | 20010824 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR | | | | |

PRIORITY APPLN. INFO.:
US 2000-227866P P 20000824
US 2001-264647P P 20010126
US 2001-300111P P 20010622
WO 2001-US26685 W 20010824

AB The present invention relates to clusters of plant genes that are regulated in response to one or more stress conditions, including cold stress, osmotic stress, and saline stress. The present invention also relates to isolated plant stress-regulated genes, including portions thereof comprising a coding sequence or a regulatory element, and to consensus sequences comprising a plant stress-regulated regulatory element. A GeneChip.tautm. Arabidopsis Genome Array was used to identify clusters of genes that were coordinately induced in response to various stress conditions, using probes synthesized in situ designed to measure temporal and spatial gene expression of .apprx.8700 genes in greater than 100 EST clusters. Of the .apprx.8700 nucleotides sequences represented on the array, 2862 nucleotide sequences showed at least a 2-fold change in expression in at least one sample relative to no-treatment controls in A. thaliana. In addn., the invention relates to a recombinant polynucleotide, which includes a plant stress-regulated gene, or functional portion thereof, operatively linked to a

heterologous nucleotide sequence. The invention further relates to a transgenic plant, which contains a plant stress-regulated gene or functional portion thereof that was introduced into a progenitor cell of the plant. In addn., the invention relates to methods of using a plant stress-regulated gene to confer upon a plant a selective advantage to a stress condition. The invention also relates to a method of identifying an agent that modulates the activity of a plant stress-regulated regulatory element.

L5 ANSWER 6 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:505738 HCAPLUS
DOCUMENT NUMBER: 137:258374
TITLE: The p66Shc longevity gene is silenced through epigenetic modifications of an alternative promoter
AUTHOR(S): Ventura, Andrea; Luzi, Lucilla; Pacini, Sonia; Baldari, Cosima T.; Pelicci, Pier Giuseppe
CORPORATE SOURCE: Department of Experimental Oncology, European Institute of Oncology, Milan, 20141, Italy
SOURCE: Journal of Biological Chemistry (2002), 277(25), 22370-22376
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The mammal Shc locus encodes three overlapping isoforms (46, 52, and 66 kDa) that differ in the length of their N-terminal regions. P46/p52Shc and p66Shc have been implicated, resp., in the cytoplasmic propagation of growth and apoptogenic signals. Levels of p66Shc expression correlate with life span duration in mice. P46Shc and p52Shc are ubiquitously expressed, whereas p66Shc is expressed in a cell lineage-specific fashion. However, the mechanisms underlying the regulation of Shc protein expression are unknown. Here we report the identification of two alternative promoters, driving the transcription of two mRNAs coding for p46/p52Shc and p66Shc. We show that treatment with an inhibitor of histone deacetylases or with a demethylating agent results in induction of p66Shc expression in cells that normally do not express this isoform but leaves the levels of the two other isoforms unchanged. Moreover, anal. of the methylation pattern of the p66Shc promoter in a panel of primary and immortalized human cells showed inverse correlation between p66Shc expression and methylation d. of its promoter. These results identify histone deacetylation and cytosine methylation as the mechanisms underlying p66Shc silencing in nonexpressing cells.
IT **434273-42-4**, GenBank AF455140
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; p66Shc longevity gene is silenced through epigenetic modifications of an alternative promoter)
REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 7 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:483007 HCAPLUS
DOCUMENT NUMBER: 137:42660

TITLE: Protein, gene and cDNA sequence of human and mouse Box-dependent Myc-interacting protein (Bin1) and uses in cancer diagnosis

INVENTOR(S): Prendergast, George C.; Sakamuro, Daitoku
PATENT ASSIGNEE(S): The Wistar Institute of Anatomy and Biology, USA

SOURCE: U.S., 64 pp., Cont.-in-part of U. S. 6,048,702.
CODEN: USXXAM

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| US 6410238 | B1 | 20020625 | US 1999-445247 | 19991203 |
| US 6048702 | A | 20000411 | US 1997-870126 | 19970606 |
| WO 9855151 | A1 | 19981210 | WO 1998-US11647 | 19980604 |

W: AU, CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.:
US 1997-870126 A2 19970606
WO 1998-US11647 W 19980604
US 1995-435454 A2 19950505
US 1996-652972 A2 19960524

AB The present invention provides human Bin1 genomic sequences and proteins encoded thereby. Also provided are compns. and methods utilizing these sequences and proteins in the diagnosis and treatment of cancers and hyperplastic disease states. Further provided are oligonucleotides derived from sequences encoding Bin1, as well as compns. and methods utilizing same for diagnostic and therapeutic purposes. The invention also relates to protein and cDNA sequence of human and mouse Box-dependent Myc-interacting protein (Bin1). The invention demonstrated that the assocn. between GST-Bin1 fusion protein and Myc was both specific and physiol. relevant, since it depended upon the presence of the Myc boxes. A set of deletion mutant of Bin1 was constructed to study the inhibition of Bin1 on oncogenic effect of transcription factor E1A and mutant p53 protein. The domains required to inhibit E1A and mutant p53 were overlapping, but distinct, and in each case different from those required to block Myc, implying that Bin1 could inhibit Myc-independent transformation through two mechanisms that required U1 or the SH3 domain, resp. In normal cells where growth in regulated, Bin1 is located primarily in the nucleoplasm but a fraction of the protein is locate in a subnuclear punctate compartment(s). However, in tumor cells, where growth is deregulated, the punctate localization predominates, suggesting that Bin1 localization is assocd. with growth regulatory capability.

IT **438516-84-8**
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; protein, gene and cDNA sequence of human and mouse Box-dependent Myc-interacting protein (Bin1) and uses in cancer diagnosis)

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 8 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:501197 HCAPLUS
DOCUMENT NUMBER: 138:181862
TITLE: Regulation of the pancreatic pro-endocrine gene Neurogenin3. [Erratum to document cited in CA136:146041]
AUTHOR(S): Lee, Jane C.; Smith, Stewart B.; Watada, Hirotaka; Lin, Joseph; Scheel, David; Wang, Juehu; Mirmira, Reghavendra G.; German, Michael S.
CORPORATE SOURCE: Hormone Research Institute and the Deepartment of Pediatrics, University of California, San Francisco, CA, 94143, USA
SOURCE: Diabetes (2001), 50(7), 1675
CODEN: DIAEAZ; ISSN: 0012-1797
PUBLISHER: American Diabetes Association
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The authors would like to acknowledge receipt of the National Institutes of Health Grant DK07161 (to J.C.L.).
IT **390513-25-4**, GenBank AF234829
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(regulation of pancreatic pro-endocrine neurogenin3 gene in human and mouse (Erratum))

L5 ANSWER 9 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:490372 HCAPLUS
DOCUMENT NUMBER: 136:146041
TITLE: Regulation of the pancreatic pro-endocrine gene neurogenin3
AUTHOR(S): Lee, Jane C.; Smith, Stewart B.; Watada, Hirotaka; Lin, Joseph; Scheel, David; Wang, Juehu; Mirmira, Raghavendra G.; German, Michael S.
CORPORATE SOURCE: Hormone Research Institute and the Department of Pediatrics, University of California, San Francisco, CA, 94143, USA
SOURCE: Diabetes (2001), 50(5), 928-936
CODEN: DIAEAZ; ISSN: 0012-1797
PUBLISHER: American Diabetes Association
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Neurogenin3 (ngn3), a basic helix-loop-helix (bHLH) transcription factor, functions as a pro-endocrine factor in the developing pancreas: by itself, it is sufficient to force undifferentiated pancreatic epithelial cells to become islet cells. Because ngn3 expression dets. which precursor cells will differentiate into islet cells, the signals that regulate ngn3 expression control islet cell formation. To investigate the factors that control ngn3 gene expression, we mapped the human and mouse ngn3 promoters and delineated transcriptionally active sequences within the human promoter. Surprisingly, the human ngn3 promoter drives transcription in all cell lines tested, including fibroblast cell lines. In contrast, in transgenic animals the promoter drives expression specifically in regions of ngn3 expression in the developing pancreas and gut; and the addn. of distal sequences greatly enhances transgene expression. Within the distal enhancer,

binding sites for several pancreatic transcription factors, including hepatocyte nuclear factor (HNF)-1 and HNF-3, form a tight cluster. HES1, an inhibitory bHLH factor activated by Notch signaling, binds to the proximal promoter and specifically blocks promoter activity. Together with previous genetic data, these results suggest a model in which the ngn3 gene is activated by the coordinated activities of several pancreatic transcription factors and inhibited by Notch signaling through HES1.

IT **390513-25-4**, GenBank AF234829
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; regulation of pancreatic pro-endocrine neurogenin3 gene in human and mouse)

REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 10 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:322774 HCAPLUS
DOCUMENT NUMBER: 136:49212
TITLE: Expression of the human **.beta.3-adrenergic** receptor gene in SK-N-MC cells is under the control of a distal enhancer
AUTHOR(S): Susulic, Vedrana S.; LaVallette, Lucille; Duzic, Emir; Chen, Liang; Shuey, David; Karathanasis, Sotirios K.; Steiner, Kurt E.
CORPORATE SOURCE: Metabolic Diseases Department, Wyeth-Ayerst Laboratories, Inc., Princeton, NJ, 08543, USA
SOURCE: Endocrinology (2001), 142(5), 1935-1949
CODEN: ENDOAO; ISSN: 0013-7227
PUBLISHER: Endocrine Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Mechanisms of **transcriptional regulation** of the human **.beta.3-adrenergic** receptor were studied using SK-N-MC cells, a human neuroblastoma cell line that expresses .beta.3- and .beta.1-adrenergic receptors endogenously. Deletions spanning different portions of a 7-kb 5'-flanking region of the human **.beta.3-adrenergic** receptor gene were linked to a luciferase reporter and transfected in SK-N-MC, CV-1, and HeLa cells. Maximal luciferase activity was obsd. when a 200-bp region located between -6.5 and -6.3 kb from the translation start site was present. This region functioned only in SK-N-MC cells. Electrophoretic mobility shift assays of nuclear exts. from SK-N-MC, CV-1, and HeLa cells using double stranded oligonucleotides spanning different portions of the 200-bp region as probes and transient transfection studies revealed the existence of three cis-acting regulatory elements: -6.468 kb-AGGTGGACT- -6.458 kb, -6.448 kb-GCCTCTCTGGGGAGCAGCTTCTCC-6.428 kb, and -6.405 kb-20 repeats of CCTT-6.385 kb. These elements act together to achieve full transcriptional activity. Mutational anal., antibody supershift, and electrophoretic mobility shift assay competition expts. indicated that element A binds the transcription factor Sp1, element B binds protein(s) present only in nuclear exts. from SK-N-MC cells and brown adipose tissue, and element C binds protein(s) present in both SK-N-MC and HeLa cells. In addn., element C exhibits characteristics of an S1 nuclease-hypersensitive

site. These data indicate that cell-specific pos. cis-regulatory elements located 6.5 kb upstream from the translation start site may play an important role in **transcriptional regulation** of the human **.beta.3-adrenergic** receptor. These data also suggest that brown adipose tissue-specific transcription factor(s) may be involved in the tissue-specific expression of the **.beta.3-adrenergic** receptor gene.

IT **336679-97-1**, GenBank AF359565
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(expression of the human **.beta.3-adrenergic** receptor gene in SK-N-MC cells is under the control of a distal enhancer)

REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 11 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:824895 HCAPLUS
DOCUMENT NUMBER: 135:132953
TITLE: The gene encoding rat 3-phosphoglycerate dehydrogenase
AUTHOR(S): Robbi, Mariette; Achouri, Younes; Szpirer, Claude; Van Schaftingen, Emile
CORPORATE SOURCE: Laboratoire de Chimie Physiologique, Christian de Duve Institute of Cellular Pathology and Universite Catholique de Louvain, Brussels, B-1200, Belg.
SOURCE: Mammalian Genome (2000), 11(11), 1034-1036
CODEN: MAMGEC; ISSN: 0938-8990
PUBLISHER: Springer-Verlag New York Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The enzyme 3-phosphoglycerate dehydrogenase (PHGDH) catalyzes the first step in serine biosynthesis and is present in prokaryotes and eukaryotes. There is some evidence for **transcriptional regulation** of the gene for PHGDH in rat liver and in proliferating cells. The authors have cloned and sequenced genomic DNA which encodes the rat 3-phosphoglycerate dehydrogenase gene (Phgdh) and about 5 kb of upstream DNA. Thirteen exons were identified, including an exon 1' which is only expressed in testis due to RNA splicing and does not affect the amino acid sequence. A no. of transcription start sites were identified that were not tissue-specific or suggestive of more than one promoter. The rat gene Phgdh was mapped to 2q34 using mouse x rat cell hybrids and FISH (fluorescence in situ hybridization). The 5'-flanking region was analyzed for promoter activity by transfecting FTO2B hepatoma cells with rat gene Phgdh DNA fragments fused to a luciferase reporter gene. A region with promoter activity was identified between nucleotides -1560 and -765.

IT **263952-68-7**, GenBank AJ271975
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; of genomic DNA encoding rat 3-phosphoglycerate dehydrogenase)

REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE

FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 12 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:564473 HCAPLUS
DOCUMENT NUMBER: 134:66939
TITLE: Alternative exon usage of rat septins
AUTHOR(S): Jackisch, Bjorn-Oliver; Hausser, Heinz; Schaefer, Liliana; Kappler, Joachim; Muller, Hans Werner; Kresse, Hans
CORPORATE SOURCE: Department of Internal Medicine, Institute of Physiological Chemistry and Pathobiochemistry, University of Munster, Munster, D-48149, Germany
SOURCE: Biochemical and Biophysical Research Communications (2000), 275(1), 180-188
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Septins represent a family of phylogenetically conserved proteins required for cytokinesis. Their presence in pre- and postsynaptic neuronal membranes suggests a general function as scaffolds for membrane reorganization. The **transcriptional regulation** of all septins examd. so far is complex, resulting in alternatively spliced variants. We focus here on the rat homolog of the gene for the human septin MSF, a truncated form of which, designated eseptin, had been described previously. It will be shown here that there is an alternative usage of the first exon by two forms, named exon r1a and r1b, resp. Exon r1a, but not exon r1b, contains a part of the coding sequence while the start of translation for the remaining coding sequence resides in the second exon. The complete genomic organization was resolved and data on the temporal and spatial expression of this septins are presented. (c) 2000 Academic Press.
IT **244895-16-7**, GenBank AF170253 **244895-31-6**, GenBank AF173899
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; alternative exon usage of rat septins)
REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 13 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:535280 HCAPLUS
DOCUMENT NUMBER: 133:145940
TITLE: **Transcriptional regulation** of the human **.beta.3-adrenergic** receptor gene
INVENTOR(S): Susulic, Vedrana S.; Duzic, Emir
PATENT ASSIGNEE(S): American Home Products Corporation, USA
SOURCE: PCT Int. Appl., 88 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 2000044901 | A1 | 20000803 | WO 2000-US2632 | 20000201 |
| W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | | |
| US 6197580 | B1 | 20010306 | US 1999-243335 | 19990201 |
| CA 2360064 | AA | 20000803 | CA 2000-2360064 | 20000201 |
| EP 1147191 | A1 | 20011024 | EP 2000-905905 | 20000201 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | | |
| JP 2002535005 | T2 | 20021022 | JP 2000-596143 | 20000201 |
| US 2002102552 | A1 | 20020801 | US 2001-761116 | 20010116 |

PRIORITY APPLN. INFO.: US 1999-243335 A 19990201
WO 2000-US2632 W 20000201

AB The present invention relates to a pos. cis-regulatory (enhancer) element and trans-acting (activating) factor for the **transcriptional regulation** of human **.beta .3-adrenergic** receptor (**.beta. 3-AR**) gene. A region localized between -6.50 and -6.30 kb of the proximal promoter contg. three segments that act synergistically to achieve full transcriptional activity is identified as the regulatory elements responsible for tissue-specific **transcriptional regulation** of human **.beta.3-AR**. One segment, termed segment A, contains an Sp1 binding site. Another of the sequences, termed segment B, is a binding site for a trans-acting factor present in cells that constitutively express **.beta. 3-AR**. The third segment, C, is an S1 nuclease-sensitive site having CCTT repeats. In a specific embodiment, the trans-acting factor is expressed in neuroblastoma (SK-N-MC) and brown adipose tissue cells, but little or not at all in CV-1, HeLa, or white adipose tissue cells. Recombinant vectors under control of this **transcriptional regulation** region, particularly contg. the B and C segments, provide a substrate for high throughput assays, such as reporter gene assays, to identify compds. that can increase the level of expression of **. beta.3-AR**. The B segment nucleic acids also provide for isolation and cloning of the trans-acting factor. Mechanisms of **transcriptional regulation** and identification of other adjacent proteins involved in the regulation of the h.**beta.3-AR** gene expression are provided.

IT **287496-21-3**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(S1 nuclease sensitive site of h.**beta.3-AR** gene; **transcriptional regulation** of human **.beta.3-adrenergic** receptor gene)

IT **287496-35-9**

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; **transcriptional regulation** of human **.beta.3-adrenergic** receptor gene)

IT **287496-84-8 287496-89-3 287496-90-6 287496-91-7**
RL: PRP (Properties)
(unclaimed nucleotide sequence; **transcriptional regulation** of the human **.beta.3-adrenergic** receptor gene)

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 14 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:405968 HCAPLUS
DOCUMENT NUMBER: 133:318161
TITLE: A 66-Base-Pair Enhancer Module Activates the Expression of a Distinct Isoform of UDP-glucuronosyltransferase Family 1 (UGT1A2) in Primary Hepatocytes
AUTHOR(S): Emi, Yoshikazu; Ohnishi, Aki; Kajimoto, Takahiro; Ikushiro, Shin-ichi; Iyanagi, Takashi
CORPORATE SOURCE: Department of Life Science, Himeji Institute of Technology, Hyogo, 678-1297, Japan
SOURCE: Archives of Biochemistry and Biophysics (2000), 378(2), 384-392
CODEN: ABBIA4; ISSN: 0003-9861
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB UGT1A2, an isoform of the UDP-glucuronosyltransferase family 1 (UGT1), is not expressed in the rat liver, but its expression was highly induced in primary cultures of rat hepatocytes. In primary hepatocytes that had been cultured for 70 h, the amt. of UGT1A2 mRNA was 100 times higher than that in the rat liver. Deletion anal. of a 4.8-kb promoter region of the UGT1A2 gene revealed that a 66-nucleotide region between -307 and -242 upstream of the transcription start site was required for induction of UGT1A2 expression. The 66-nucleotide region acted on a heterologous promoter in a manner independent of its position and orientation in reporter constructs. Gel mobility shift assay showed that a specific binding protein to this region appeared in the nuclei of cultured hepatocytes, but was not present in the rat liver. DNase I protection anal. revealed the existence of a CTGGCAC core sequence between -274 and -268 of the UGT1A2 promoter. Methylation interference assay showed that the guanine residues at -294 and -287 on the upper strand and the guanine residue at -267 on the lower strand as well as the core sequence were required for the DNA-protein interaction. These results suggest that the 66-nucleotide region, which was designated culture-assocd. expression responsive enhancer module (CEREM), interacts with a specific nuclear protein and enhances the expression of UGT1A2 in cultured hepatocytes. (c) 2000 Academic Press.

IT **261334-62-7**, GenBank AB025923
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL

(Biological study)
(nucleotide sequence; 66-Base-Pair Enhancer Module Activates Expression of Distinct Isoform of UDP-glucuronosyltransferase Family 1 (UGT1A2) in Primary Hepatocytes)
REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 15 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:134182 HCAPLUS
DOCUMENT NUMBER: 132:304235
TITLE: Characterization of the c-specific promoter of the gene encoding human endothelin-converting enzyme-1 (ECE-1)
AUTHOR(S): Funke-Kaiser, H.; Bolbrinker, J.; Theis, S.; Lemmer, J.; Richter, C.-M.; Paul, M.; Orzechowski, H.-D.
CORPORATE SOURCE: Institute of Clinical Pharmacology and Toxicology, Benjamin Franklin Medical Center, Freie Universitat Berlin, Berlin, 12200, Germany
SOURCE: FEBS Letters (2000), 466(2,3), 310-316
CODEN: FEBLAL; ISSN: 0014-5793
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Human ECE-1 is expressed in four isoforms with different tissue distribution and its mRNA and protein levels are altered under certain pathophysiol. conditions. To investigate the **transcriptional regulation** of ECE-1, we studied the regulatory region of ECE-1c, the major ECE-1 isoform. A genomic clone comprising the complete human ECE-1 gene including the putative ECE-1c-specific promoter was obtained. Up to 968 bp upstream of the putative c-specific translation initiation start codon and several serial deletion mutants were subcloned into a reporter vector and transfected into endothelial (BAEC, EA.hy926, ECV304) and epithelial (MDA MB435S, MCF7) cells, showing very strong promoter activity in comparison to the SV40 promoter and to the previously described ECE-1a and 1b promoters. Transfection of serial deletion mutants indicated two pos. regulatory regions within the promoter (-142/-240 and -240/490) likely involved in binding GATA and ETS transcription factors. RNase protection assay (RPA) and 5'-RACE revealed multiple transcriptional start sites located at about -110, -140 and -350 bp. Site-directed mutagenesis demonstrated a crucial role for the E2F cis-element for basal ECE-1c promoter activity. Addnl., we found a correlation between isoform-specific ECE-1 mRNA levels and corresponding ECE-1a, 1b, 1c promoter activities.
IT **217120-85-9**, GenBank AL031728
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(nucleotide sequence; characterization of c-specific promoter of the gene encoding human endothelin-converting enzyme-1)
REFERENCE COUNT: 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 16 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:784257 HCAPLUS

DOCUMENT NUMBER: 132:31783
TITLE: Sequence of human homologue of unc-53 protein of C. elegans with therapeutic applications
INVENTOR(S): Luyten, Walter Herman Maria Louis; De Raeymaeker, Marc Carl; Geysen, Johan Jozef Gustave Hendrik; Bogaert, Thierry A. O. E.; Maerten, Luc Jacques Simon; Verhassèlt, Peter; Van de Craen, Marc
PATENT ASSIGNEE(S): Janssen Pharmaceutica N.V., Belg.
SOURCE: PCT Int. Appl., 147 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|---|---|---|---|
| WO 9963080 | A1 | 19991209 | WO 1999-EP3848 | 19990602 |
| W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | | |
| RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG | | | | |
| CA 2330179 | AA | 19991209 | CA 1999-2330179 | 19990602 |
| AU 9943735 | A1 | 19991220 | AU 1999-43735 | 19990602 |
| EP 1092019 | A1 | 20010418 | EP 1999-926511 | 19990602 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | | |

PRIORITY APPLN. INFO.: GB 1998-11962 A 19980603
WO 1999-EP3848 W 19990602

AB There is disclosed human homologues of the UNC-53 protein of C. elegans and cDNA sequences coding for said homologues or functional equiv. thereof. The invention also relates to processes for identifying compds. which control cell behavior, compds. identified and pharmaceutical compns. contg. them in addn. to processes and assays for identifying disease states in which said gene or protein is dysfunctional. The UNC-53 protein is differentially expressed in different parts of the brain. Splice variants of UNC-53 protein were found also. A non-silent single nucleotide polymorphism in Hunc-53/1 in position 1232 and in Hs-unc-53/2 in position 929 was found. This indicates that variations exist in human unc-53s which-in some cases- may be relevant to the proper functioning of the UNC-53 protein and hence in disease. Alternative 5'-start exons were also found. This gene Hs-UNC-53/2 is located on human chromosome 11. The hs-unc-53/3 gene was mapped on chromosome 12q21.1. F-actin reorganization and microtubule binding of Hs-UNC-53/3 was reported also. Compd. screens which affect the function of human UNC-53 protein were measured by lamellipodia formation. Transgenic systems for expression of this protein are reported to alter cell migration by creating a mutation in the UNC-53 protein. Methods as described above and manuf. of a medicament for promoting neuronal regeneration, revascularization, wound healing, or treatment of chronic neurodegenerative diseases or

acute traumatic injuries or fibrotic disease or autoimmune diseases such as rheumatoid arthritis and sclerosis. Methods to screen for other proteins involved in signal transduction are provided. Antisense RNA and DNA are also given.

IT **252323-74-3**
RL: PRP (Properties)
(unclaimed sequence; sequence of human homolog of unc-53 protein of C. elegans with therapeutic applications)

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 17 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:800726 HCAPLUS
DOCUMENT NUMBER: 128:124353
TITLE: Structural analysis of the human BIN1 gene. Evidence for tissue-specific **transcriptional regulation** and alternate RNA splicing
AUTHOR(S): Wechsler-Reya, Robert; Sakamuro, Daitoku; Zhang, Jing; Duhadaway, James; Prendergast, George C.
CORPORATE SOURCE: The Wistar Institute, Philadelphia, PA, 19104, USA
SOURCE: Journal of Biological Chemistry (1997), 272(50), 31453-31458
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB BIN1 is a putative tumor suppressor that was identified through its interaction with the MYC oncoprotein. To begin to identify elements of BIN1 whose alteration may contribute to malignancy, we cloned and characterized the human BIN1 gene and promoter. Nineteen exons were identified in a region of >54 kilobases, six of which were alternately spliced in a cell type-specific manner. One alternately spliced exon encodes part of the MYC-binding domain, suggesting that splicing controls the MYC-binding capacity of BIN1 polypeptides. Four other alternately spliced exons encode amphiphysin-related sequences that were included in brain-specific BIN1 species, also termed amphiphysin isoforms or amphiphysin II. The 5'-flanking region of BIN1 is GC-rich and lacks a TATA box but directs transcriptional initiation from a single site. A .apprx.0.9-kilobase fragment from this region was sufficient for basal transcription and transactivation by MyoD, which may account for the high levels of BIN1 obsd. in skeletal muscle. This study lays the foundation for genetic and epigenetic investigations into the role of BIN1 in normal and neo-plastic cell regulation.

IT **202053-19-8**
RL: PRP (Properties)
(nucleotide sequence; structural anal. of the human BIN1 gene: evidence for tissue-specific **transcriptional regulation** and alternate RNA splicing)

L5 ANSWER 18 OF 19 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1996:429941 HCAPLUS
DOCUMENT NUMBER: 125:134562
TITLE: Characterization of msim, a murine homolog of

the Drosophila sim transcription factor

AUTHOR(S): Moffett, Peter; Dayo, Mabel; Reece, Mark; McCormick, Mary Kay; Pelletier, Jerry

CORPORATE SOURCE: Dep. of Biochemistry and McGill Cancer Center, McGill Univ., Montreal, QC, H3G 1Y6, Can.

SOURCE: Genomics (1996), 35(1), 144-155
CODEN: GNMCEP; ISSN: 0888-7543

PUBLISHER: Academic

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Mutations in the Drosophila single-minded (sim) gene result in loss of precursor cells that give rise to midline cells of the embryonic central nervous system. During the course of an exon-trapping strategy aimed at identifying transcripts that contribute to the etiol. and pathophysiol. of Down syndrome, we identified a human exon from the Down syndrome crit. region showing significant homol. to the Drosophila sim gene. Using a cross-hybridization approach, we have isolated a murine homolog of the Drosophila sim gene, which we designated msim. Nucleotide and predicted amino acid sequence analyses of msim cDNA clones indicate that this gene encodes a member of the basic-helix-loop-helix class of transcription factors. The murine and Drosophila proteins share 88% residues within the basic-helix-loop-helix domain, with an overall homol. of 92%. In addn., the N-terminal domain of MSIM contains two PAS dimerization motifs also featured in the Drosophila sim gene product, as well as a small no. of other transcription factors. Northern blot anal. of adult murine tissues revealed that the msim gene produces a single mRNA species of .apprx.4 kb expressed in a small no. of tissues, with the highest levels in the kidneys and lower levels present in skeletal muscle, lung, testis, brain, and heart. In situ hybridization expts. demonstrate that msim is also expressed in early fetal development in the central nervous system and in cartilage primordia. The characteristics of the msim gene are consistent with its putative function as a **transcriptional regulator.**

IT **177643-91-3,** GenBank U42554
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(nucleotide sequence; and mapping of mouse gene msim, the human homolog of which maps to the Down syndrome crit. region)

L5 ANSWER 19 OF 19 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1996:152631 HCAPLUS

DOCUMENT NUMBER: 124:256565

TITLE: Expression patterns of two murine homologs of Drosophila single-minded suggest possible roles in embryonic patterning and in the pathogenesis of Down syndrome

AUTHOR(S): Fan, Chen-Ming; Kuwana, Ellen; Bulfone, Alessandro; Fletcher, Colin F.; Copeland, Neal G.; Jenkins, Nancy A.; Crews, Stephen; Martinez, Salvador; Puelles, Luis; et al.

CORPORATE SOURCE: Howard Hughes Med. Inst., Univ. California, San Francisco, CA, 94143-0452, USA

SOURCE: Molecular and Cellular Neuroscience (1996), 7(1), 1-16
CODEN: MOCNED; ISSN: 1044-7431

PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The single-minded (sim) gene encodes a **transcriptional regulator** that functions as a key determinant of central nervous system (CNS) midline development in Drosophila. The authors report here the identification of two murine homologs of sim, Sim1 and Sim2, whose products show a high degree of sequence conservation with Drosophila SIM in their amino-terminal halves, with each contg. a basic helix-loop-helix domain as well as a PAS domain. Sim1 maps to the proximal region of mouse chromosome 10, whereas Sim2 maps to a portion of the distal end of chromosome 16 that is syntenic to the Down syndrome crit. region of human chromosome 21. Recent exon-trapping studies have identified in the crit. region several exons of a human sim homolog which appears to be the homolog of murine Sim2; this has led to the hypothesis that increased dosage of this sim homolog in cases of trisomy 21 might be a causal factor in the pathogenesis of Down syndrome. The authors have examd. the expression patterns of the Sim genes during embryogenesis. Both genes are expressed in dynamic and selective fashion in specific neuromeric compartments of the developing forebrain, and the expression pattern of Sim2 provides evidence for early regionalization of the diencephalon prior to any overt morphol. differentiation in this region. Outside the CNS, Sim1 is expressed in mesodermal and endodermal tissues, including developing somites, mesonephric duct, and foregut. Sim2 is expressed in facial and trunk cartilage, as well as trunk muscles. Both murine Sim genes are also expressed in the developing kidney. The data suggest that the Sim genes play roles in directing the regionalization of tissues where they are expressed. Moreover, the expression pattern documented for Sim2 may provide insights into its potential roles in Down syndrome.

IT **174098-94-3**, GenBank U40576
RL: PRP (Properties)
(nucleotide sequence; developmental expression, chromosomal localization, and cDNA sequence of Sim1 and Sim2 genes of mouse)

E1 THROUGH E27 ASSIGNED

FILE 'REGISTRY' ENTERED AT 16:13:28 ON 12 JUN 2003
L6 27 SEA FILE=REGISTRY ABB=ON PLU=ON (390513-25-4/BI OR 174098-94-3/BI OR 177643-91-3/BI OR 202053-19-8/BI OR 217120-85-9/BI OR 227594-62-9/BI OR 244895-16-7/BI OR 244895-31-6/BI OR 252323-74-3/BI OR 258491-28-0/BI OR 261334-62-7/BI OR 263952-68-7/BI OR 266660-95-1/BI OR 267626-85-7/BI OR 287496-21-3/BI OR 287496-35-9/BI OR 287496-84-8/BI OR 287496-89-3/BI OR 287496-90-6/BI OR 287496-91-7/BI OR 336679-97-1/BI OR 385252-57-3/BI OR 389189-05-3/BI OR 391788-88-8/BI OR 392013-60-4/BI OR 434273-42-4/BI OR 438516-84-8/BI)

=> s l6 and l1
L7 27 L6 AND L1

L7 ANSWER 1 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **438516-84-8** REGISTRY
CN DNA (human gene Bin1 exon 7-12A plus flanks) (9CI) (CA INDEX NAME)

OTHER NAMES:
CN 11: PN: US6410238 SEQID: 11 claimed DNA
SQL 8051
MF Unspecified
CI MAN

REFERENCE 1: 137:42660

L7 ANSWER 2 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **434273-42-4** REGISTRY
CN DNA (mouse strain 129/SvJ Src homolog 2 domain-containing transforming protein 1 isoform p66 gene plus Src homolog 2 domain-containing transforming protein 1 isoform p52 gene) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF455140
SQL 5178
MF Unspecified
CI MAN

REFERENCE 1: 137:258374

L7 ANSWER 3 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **392013-60-4** REGISTRY
CN GenBank AC002400 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3: PN: WO03008647 TABLE: 13b unclaimed DNA
CN 507: PN: WO02070737 FIGURE: 6 unclaimed DNA
SQL 138839
MF Unspecified
CI MAN

REFERENCE 1: 138:148639

REFERENCE 2: 137:246071

L7 ANSWER 4 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **391788-88-8** REGISTRY
CN DNA (human clone Qc-9D3 ) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1011: PN: WO0224956 FIGURE: 5 claimed DNA
CN 15: PN: WO03027633 TABLE: 6 unclaimed DNA
CN 967: PN: WO03003906 TABLE: 5A unclaimed DNA
CN DNA (human clone QLL-D9139, Qc-7G12, Qc-7C1, Qc-12B2, Qc-12D5, QLL-A074, Qc-9D3)
CN GenBank U52112
SQL 181343
MF Unspecified
CI MAN

REFERENCE 1: 138:283693

REFERENCE 2: 138:266967

REFERENCE 3: 138:266966

REFERENCE 4: 138:266965

REFERENCE 5: 138:168793

REFERENCE 6: 138:168236

REFERENCE 7: 138:67954

REFERENCE 8: 138:50950

REFERENCE 9: 137:347543

REFERENCE 10: 137:45438

L7 ANSWER 5 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **390513-25-4** REGISTRY
CN DNA (human gene ngn3 plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN DNA (human neurogenin-3 gene ngn3 plus flanks)
CN GenBank AF234829
SQL 5340
MF Unspecified
CI MAN

REFERENCE 1: 138:199856

REFERENCE 2: 138:181862

REFERENCE 3: 136:146041

L7 ANSWER 6 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **389189-05-3** REGISTRY
CN DNA (human clone lambda A3. ) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2102: PN: WO02059377 TABLE: 13 claimed DNA
CN 921: PN: WO0224956 FIGURE: 4 claimed DNA
CN DNA (human clone lambda A3. aldolase A gene)
CN GenBank X12447
SQL 7530
MF Unspecified
CI MAN

REFERENCE 1: 137:244289

REFERENCE 2: 137:45438

L7 ANSWER 7 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **385252-57-3** REGISTRY
CN DNA (human clone HG3925 gene KIAA0537 protein kinase cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 118: PN: WO02070737 FIGURE: 6 unclaimed DNA
CN 47: PN: WO02063037 TABLE: 1 unclaimed DNA
CN DNA (human brain clone HG3925 gene KIAA0537 AMPK-family protein kinase ARK5 cDNA plus flanks)
CN DNA (human clone HG3925 gene KIAA0537 cDNA)
CN GenBank AB011109
SQL 6828
MF Unspecified
CI MAN

REFERENCE 1: 138:316554

REFERENCE 2: 137:246071

REFERENCE 3: 137:180730

L7 ANSWER 8 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **336679-97-1** REGISTRY
CN DNA (human .beta.3-adrenergic receptor gene promoter region-containing fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF359565
SQL 7127
MF Unspecified
CI MAN

REFERENCE 1: 136:49212

L7 ANSWER 9 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **287496-91-7** REGISTRY
CN DNA, d(G-A-T-C-C-G-C-C-T-C-T-G-G-G-G-A-G-C-A-G-C-T-T-G-A-G-G-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 48: PN: WO0044901 SEQID: 48 unclaimed DNA
SQL 28
MF Unspecified
CI MAN

REFERENCE 1: 133:145940

L7 ANSWER 10 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **287496-90-6** REGISTRY
CN DNA, d(G-A-T-C-C-G-C-C-T-C-T-G-G-G-G-A-G-C-A-G-G-A-A-C-T-C-C-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 47: PN: WO0044901 SEQID: 47 unclaimed DNA
SQL 28
MF Unspecified
CI MAN

REFERENCE 1: 133:145940

L7 ANSWER 11 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **287496-89-3** REGISTRY
CN DNA, d(G-A-T-C-C-G-C-C-T-C-T-G-G-G-G-A-G-G-T-C-C-T-T-C-T-C-C-A) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 46: PN: WO0044901 SEQID: 46 unclaimed DNA
SQL 28
MF Unspecified
CI MAN

REFERENCE 1: 133:145940

L7 ANSWER 12 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **287496-84-8** REGISTRY
CN DNA, d(G-A-T-C-C-G-C-C-T-C-T-G-G-G-G-A-G-C-A-G-C-T-T-C-T-C-C-A)

(9CI) (CA INDEX NAME)
OTHER NAMES:
CN 41: PN: WO0044901 SEQID: 41 unclaimed DNA
SQL 28
MF Unspecified
CI MAN

REFERENCE 1: 133:145940

L7 ANSWER 13 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **287496-35-9** REGISTRY
CN DNA (human .beta.3 adrenoceptor gene 200-bp 20 CCTT repeat-containing 5'-flanking fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3: PN: WO0044901 SEQID: 3 claimed DNA
SQL 200
MF Unspecified
CI MAN

REFERENCE 1: 133:145940

L7 ANSWER 14 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **287496-21-3** REGISTRY
CN DNA, d(G-C-C-T-C-T-G-G-G-G-A-G) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: WO0044901 SEQID: 1 claimed DNA
SQL 12
MF Unspecified
CI MAN

REFERENCE 1: 133:145940

L7 ANSWER 15 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **267626-85-7** REGISTRY
CN DNA (human gene GLP plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1492: PN: WO02070737 FIGURE: 6 unclaimed DNA
CN DNA (human gene GLP)
CN GenBank AF266285
SQL 21500
MF Unspecified
CI MAN

REFERENCE 1: 137:246071

REFERENCE 2: 135:117777

L7 ANSWER 16 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **266660-95-1** REGISTRY
CN DNA (human neuroligin 3 isoform gene plus neuroligin 3 isoform gene) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1414: PN: WO02070737 FIGURE: 6 unclaimed DNA
CN GenBank AF217413
SQL 32272
MF Unspecified
CI MAN

REFERENCE 1: 137:246071

L7 ANSWER 17 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **263952-68-7** REGISTRY
CN DNA (Rattus norvegicus gene Phgdh plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN DNA (Rattus norvegicus phosphoglycerate dehydrogenase gene plus flanks)
CN GenBank AJ271975
SQL 34071
MF Unspecified
CI MAN

REFERENCE 1: 135:132953

L7 ANSWER 18 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **261334-62-7** REGISTRY
CN DNA (Rattus norvegicus strain Wistar gene UGT1A2) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AB025923
SQL 4876
MF Unspecified
CI MAN

REFERENCE 1: 133:318161

L7 ANSWER 19 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **258491-28-0** REGISTRY
CN DNA (human clone RPCI-11-157G10 gene CACNA1E plus gene CACNA1E) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1426: PN: WO02070737 FIGURE: 6 unclaimed DNA
CN GenBank AF223391
SQL 316704
MF Unspecified
CI MAN

REFERENCE 1: 137:246071

L7 ANSWER 20 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **252323-74-3** REGISTRY
CN 65: PN: WO9963080 FIGURE: 1g unclaimed sequence (9CI) (CA INDEX NAME)
SQL 4984
MF Unspecified
CI MAN

REFERENCE 1: 132:31783

L7 ANSWER 21 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **244895-31-6** REGISTRY
CN DNA (Rattus norvegicus gene SLP protein SLP (septin-like protein) isoform SLP-b cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF173899
SQL 3745

MF Unspecified
CI MAN

REFERENCE 1: 134:66939

L7 ANSWER 22 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **244895-16-7** REGISTRY
CN DNA (Rattus norvegicus gene SLP protein SLP (septin-like protein) isoform SLP-a cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF170253
SQL 3869
MF Unspecified
CI MAN

REFERENCE 1: 134:66939

L7 ANSWER 23 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **227594-62-9** REGISTRY
CN DNA (human gene KvLQT1 plus gene KvLQT1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1545: PN: WO02070737 FIGURE: 6 unclaimed DNA
CN GenBank AJ006345
SQL 404123
MF Unspecified
CI MAN

REFERENCE 1: 137:246071

L7 ANSWER 24 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **217120-85-9** REGISTRY
CN DNA (human chromosome 1 clone 1071N3 74,037-nucleotide fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN DNA (human endothelin-converting enzyme-1 gene ECE1 isoenzyme c-specific promoter region-containing fragment)
CN GenBank AL031728
SQL 74037
MF Unspecified
CI MAN

REFERENCE 1: 132:304235

L7 ANSWER 25 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **202053-19-8** REGISTRY
CN DNA (human WI-38 cell gene BIN1 exons 7-12 plus flanks) (9CI) (CA INDEX NAME)
SQL 8310
MF Unspecified
CI MAN

REFERENCE 1: 130:49515

REFERENCE 2: 128:124353

L7 ANSWER 26 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **177643-91-3** REGISTRY
CN DNA (mouse clone 2B gene sim transcription factor cDNA plus flanks)

(9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (mouse clone 2B gene sim transcription factor messenger RNA-complementary plus 5'- and 3'-flanking region fragment)
OTHER NAMES:
CN DNA (mouse gene msim transcription factor MSIM cDNA and flanks)
SQL 3071
MF Unspecified
CI MAN

REFERENCE 1: 133:39066

REFERENCE 2: 125:134562

L7 ANSWER 27 OF 27 REGISTRY COPYRIGHT 2003 ACS
RN **174098-94-3** REGISTRY
CN DNA (Mus musculus strain Swiss Webster gene Sim-2 protein cDNA plus flanks) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid (Mus musculus strain Swiss Webster gene Sim2 protein messenger RNA-complementary plus 5'- and 3'-flanking region fragment)
OTHER NAMES:
CN GenBank U40576
SQL 3963
MF Unspecified
CI MAN

REFERENCE 1: 125:217812

REFERENCE 2: 124:256565

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GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 10:33:51 ; Search time 985 Seconds
(without alignments)
354.552 Million cell updates/sec

Title: US-09-761-116-1
Perfect score: 12
Sequence: 1 gcctctggggag 12

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| 1 | | 12 | 100.0 | 12 | 6 | AR137925 | AR137925 Sequence |
| 2 | | 12 | 100.0 | 28 | 6 | AR137965 | AR137965 Sequence |
| 3 | | 12 | 100.0 | 28 | 6 | AR137970 | AR137970 Sequence |
| 4 | | 12 | 100.0 | 28 | 6 | AR137971 | AR137971 Sequence |
| 5 | | 12 | 100.0 | 28 | 6 | AR137972 | AR137972 Sequence |
| 6 | | 12 | 100.0 | 130 | 9 | HSU39347 | U39347 Human MHC c |
| 7 | | 12 | 100.0 | 200 | 6 | AR137927 | AR137927 Sequence |
| 8 | | 12 | 100.0 | 208 | 11 | G04524 | G04524 human STS W |
| 9 | | 12 | 100.0 | 234 | 6 | AX244726 | AX244726 Sequence |
| 10 | c | 12 | 100.0 | 266 | 11 | G65279 | G65279 FBN1-64new |
| 11 | | 12 | 100.0 | 278 | 9 | HSNL1243D | X87489 H.sapiens g |
| 12 | c | 12 | 100.0 | 287 | 9 | HUMCW05 | D64153 Human DNA f |
| 13 | | 12 | 100.0 | 292 | 11 | G09804 | G09804 human STS C |
| 14 | c | 12 | 100.0 | 321 | 11 | HUMUT7961A | L30159 Human STS U |
| 15 | | 12 | 100.0 | 330 | 11 | G71854 | G71854 A09122834FM |
| 16 | | 12 | 100.0 | 343 | 11 | G71018 | G71018 A09122834FB |
| 17 | | 12 | 100.0 | 370 | 9 | AF366903 | AF366903 Homo sapi |
| 18 | | 12 | 100.0 | 381 | 6 | AX072790 | AX072790 Sequence |
| 19 | c | 12 | 100.0 | 384 | 10 | MMEB2AK1 | X04437 Mouse class |
| 20 | | 12 | 100.0 | 393 | 10 | AF028605 | AF028605 Rattus no |
| 21 | c | 12 | 100.0 | 403 | 4 | AB016736 | AB016736 Sus scrof |
| 22 | c | 12 | 100.0 | 403 | 4 | AB016737 | AB016737 Sus scrof |
| 23 | c | 12 | 100.0 | 403 | 4 | AB016738 | AB016738 Sus scrof |
| 24 | c | 12 | 100.0 | 403 | 4 | AB016739 | AB016739 Sus scrof |
| 25 | c | 12 | 100.0 | 403 | 4 | AB016740 | AB016740 Sus scrof |
| 26 | c | 12 | 100.0 | 403 | 4 | AB016741 | AB016741 Sus scrof |
| 27 | c | 12 | 100.0 | 403 | 4 | AB016742 | AB016742 Sus scrof |
| 28 | c | 12 | 100.0 | 403 | 4 | AB016743 | AB016743 Sus scrof |
| 29 | c | 12 | 100.0 | 403 | 4 | AB016744 | AB016744 Sus scrof |
| 30 | c | 12 | 100.0 | 403 | 4 | AB016745 | AB016745 Sus scrof |
| 31 | | 12 | 100.0 | 417 | 10 | AF028603 | AF028603 Rattus no |
| 32 | | 12 | 100.0 | 427 | 11 | G55693 | G55693 SHGC-101064 |
| 33 | | 12 | 100.0 | 432 | 10 | AF028604 | AF028604 Rattus no |
| 34 | c | 12 | 100.0 | 437 | 10 | MUSMX103 | M21106 Mouse induc |
| 35 | c | 12 | 100.0 | 439 | 4 | AB016251 | AB016251 Oryctolag |
| 36 | c | 12 | 100.0 | 534 | 4 | DOGP53A | L27630 Canis famil |
| 37 | c | 12 | 100.0 | 545 | 6 | AX312180 | AX312180 Sequence |
| 38 | | 12 | 100.0 | 548 | 8 | AY088677 | AY088677 Arabidops |
| 39 | c | 12 | 100.0 | 591 | 10 | AF300861 | AF300861 Peromyscu |
| 40 | c | 12 | 100.0 | 594 | 10 | AF300862 | AF300862 Peromyscu |
| 41 | c | 12 | 100.0 | 596 | 9 | HSA323688 | AJ323688 Homo sapi |
| 42 | c | 12 | 100.0 | 599 | 9 | HSA326032 | AJ326032 Homo sapi |
| 43 | c | 12 | 100.0 | 599 | 9 | HSA342624 | AJ342624 Homo sapi |
| 44 | | 12 | 100.0 | 606 | 9 | HSA338863 | AJ338863 Homo sapi |
| 45 | | 12 | 100.0 | 612 | 9 | HSA335324 | AJ335324 Homo sapi |

ALIGNMENTS

RESULT 1
AR137925
LOCUS AR137925 12 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 1 from patent US 6197580.
ACCESSION AR137925
VERSION AR137925.1 GI:14479434
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Susulic,V.S. and Duzic,E.
TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene
JOURNAL Patent: US 6197580-A 1 06-MAR-2001;

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FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
BASE COUNT        1 a      3 c      6 g      2 t
ORIGIN

  Query Match            100.0%;  Score 12;  DB 6;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 7.8e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          1 GCCTCTGGGGAG 12


RESULT 2
AR137965
LOCUS       AR137965                  28 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 41 from patent US 6197580.
ACCESSION   AR137965
VERSION     AR137965.1  GI:14479474
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Susulic,V.S. and Duzic,E.
  TITLE     Transcriptional regulation of the human .beta.3-adrenergic receptor
            gene
  JOURNAL   Patent: US 6197580-A 41 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT        4 a      10 c      8 g      6 t
ORIGIN

  Query Match            100.0%;  Score 12;  DB 6;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 7.1e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
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Db          6 GCCTCTGGGGAG 17


RESULT 3
AR137970
LOCUS       AR137970                  28 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 46 from patent US 6197580.
ACCESSION   AR137970
VERSION     AR137970.1  GI:14479479
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Susulic,V.S. and Duzic,E.
  TITLE     Transcriptional regulation of the human .beta.3-adrenergic receptor
            gene
  JOURNAL   Patent: US 6197580-A 46 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT        3 a      10 c      8 g      7 t
ORIGIN

  Query Match            100.0%;  Score 12;  DB 6;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 7.1e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          6 GCCTCTGGGGAG 17


RESULT 4
AR137971
LOCUS       AR137971                  28 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 47 from patent US 6197580.
ACCESSION   AR137971
VERSION     AR137971.1  GI:14479480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Susulic,V.S. and Duzic,E.
  TITLE     Transcriptional regulation of the human .beta.3-adrenergic receptor
            gene
  JOURNAL   Patent: US 6197580-A 47 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT        6 a      9 c      9 g      4 t
ORIGIN

  Query Match            100.0%;  Score 12;  DB 6;  Length 28;
  Best Local Similarity  100.0%;  Pred. No. 7.1e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          6 GCCTCTGGGGAG 17


RESULT 5
AR137972
LOCUS       AR137972                  28 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 48 from patent US 6197580.
ACCESSION   AR137972
VERSION     AR137972.1  GI:14479481
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Susulic,V.S. and Duzic,E.
  TITLE     Transcriptional regulation of the human .beta.3-adrenergic receptor
            gene
  JOURNAL   Patent: US 6197580-A 48 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
BASE COUNT        5 a      7 c      11 g      5 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 7.1e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          6 GCCTCTGGGGAG 17


RESULT 6
HSU39347
LOCUS       HSU39347                 130 bp    DNA     linear   PRI 21-MAR-1997
DEFINITION  Human MHC class I antigen HLA-C gene (HLA-Cw*0401 allele), intron
            1.
ACCESSION   U39347
VERSION     U39347.1  GI:1654171
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 130)
  AUTHORS   Cereb,N., Kong,Y., Lee,S., Maye,P. and Yang,S.Y.
  TITLE     Nucleotide sequences of MHC class I introns 1, 2, and 3 in humans
            and intron 2 in nonhuman primates
  JOURNAL   Tissue Antigens 47 (6), 498-511 (1996)
  MEDLINE   96408732
   PUBMED   8813739
REFERENCE   2  (bases 1 to 130)
  AUTHORS   Yang,S.Y. and Cereb,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-1995) Soo Yang, Immunology Program, Memorial
            Sloan-Kettering Cancer Center, 1275 York Ave, Box 41, New York, NY
            10021, USA
FEATURES             Location/Qualifiers
     source          1. .130
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p21.3"
                     /cell_line="WT100BIS B cell line"
     gene            1. .130
                     /gene="HLA-C"
     intron          1. .130
                     /gene="HLA-C"
                     /note="HLA-Cw*0401 allele"
                     /number=1
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 5.9e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db         27 GCCTCTGGGGAG 38


RESULT 7
AR137927
LOCUS       AR137927                 200 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 3 from patent US 6197580.
ACCESSION   AR137927
VERSION     AR137927.1  GI:14479436
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 200)
  AUTHORS   Susulic,V.S. and Duzic,E.
  TITLE     Transcriptional regulation of the human .beta.3-adrenergic receptor
            gene
  JOURNAL   Patent: US 6197580-A 3 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .200
                     /organism="unknown"
BASE COUNT       25 a     70 c     37 g     68 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 5.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db         61 GCCTCTGGGGAG 72


RESULT 8
G04524
LOCUS       G04524                   208 bp    DNA     linear   STS 19-OCT-1995
DEFINITION  human STS WI-4034, sequence tagged site.
ACCESSION   G04524
VERSION     G04524.1  GI:721482
KEYWORDS    STS; STS sequence; primer; sequence tagged site.
SOURCE      Homo sapiens Random genome wide STSs created from sheared whole
            human DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 208)
  AUTHORS   Hudson,T.
  TITLE     Whitehead Institute/MIT Center for Genome Research; Random Genome
            Wide STSs
  JOURNAL   Unpublished (1995)
REFERENCE   2  (bases 1 to 208)
  AUTHORS   Hudson,T.
  TITLE     Whitehead Institute/MIT Center for Genome Research; Physically
            Mapped STSs
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Thomas Hudson
            Whitehead Institute/MIT Center for Genome Research
            Whitehead Institute for Biomedical Research
            9 Cambridge Center, Cambridge MA 02142 USA
            Tel: 617 252 1900
            Fax: 617 252 1902
            Email: thudson@genome.wi.mit.edu

            Primer A: TATGGGCACTTTGAAGAGGG
            Primer B: CCCCAAGGAGAGCCATCT
            STS size: 155
            PCR Profile:
                  Presoak:
                  Denaturation:
                  Annealing: 56 degrees C
                  Polymerization:
                  PCR Cycles: 35
                  Thermal Cycler:
            Protocol:
                Template: 10 ng
                Primer: each 5 pM
                dNTPs: each 4 nM
                Taq Polymerase: 0.025 units/ul
                Total Vol: 20 ul

            Buffer:
                MgCl2: 1.5 mM
                KCl: 50 mM
                Tris-HCL: 10 mM
                pH: 9.3.
FEATURES             Location/Qualifiers
     source          1. .208
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="709_B_4; 802_B_4; 805_F_5; 851_E_2; 964_F_8;
                     921_A_10; (720,724)_A_(10,12); 304.8 cR from top of Chr15
                     linkage group"
     STS             51. .205
     primer_bind     51. .70
     primer_bind     complement(188. .205)
BASE COUNT       51 a     43 c     69 g     45 t
ORIGIN

  Query Match           100.0%;  Score 12;  DB 11;  Length 208;
  Best Local Similarity  100.0%;  Pred. No. 5.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db         14 GCCTCTGGGGAG 25


RESULT 9
AX244726
```

```
LOCUS       AX244726                234 bp    DNA     linear   PAT 28-SEP-2001
DEFINITION  Sequence 55 from Patent WO0166750.
ACCESSION   AX244726
VERSION     AX244726.1  GI:15859605
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 234)
  AUTHORS   Vogeli,G. and Wood,L.S.
  TITLE     G protein-coupled receptors
  JOURNAL   Patent: WO 0166750-A 55 13-SEP-2001;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .234
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       56 a     64 c     65 g     49 t
ORIGIN
```

[redacted]

```
  Query Match             100.0%;  Score 12;  DB 6;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        100 GCCTCTGGGGAG 111


RESULT 10
G65279/c
LOCUS       G65279                  266 bp    DNA     linear   STS 14-JUL-2000
DEFINITION  FBN1-64new Random genomic STS Homo sapiens STS genomic, sequence
            tagged site.
ACCESSION   G65279
VERSION     G65279.1  GI:9211115
KEYWORDS    STS.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 266)
  AUTHORS   Oefner,P.J.
  TITLE     Human random genomic STS survey, unpublished data
  JOURNAL   Unpublished (1999)
COMMENT
            Contact: Peter Oefner
            Stanford Genome Center
            Stanford University
            855 California Ave., Palo Alto, CA 94304, USA
            Tel: 6508121926
            Fax: 6508121975
            Email: Oefner@genome.stanford.edu
            Primer A: CCTACCTTGTCTTCCCATTCTAA
            Primer B: ACAGGAGACATCAGGAGAAACTAAC
            STS size: 266
            PCR Profile:
            Initial denaturing step of 95 degrees C for 10 min to activate
            AmplTaq Gold (1
            min for AmpliTaq);
            14 cycles of touchdown: 94 degrees C for 20 sec, annealing for 1
            min at 63
            degrees C to
            56 degrees C using decrements of 0.5 degrees C, extension at 72
            degrees C for 1
            min;
            20 cycles at 94 degrees C for 20s, 56 degrees C for 45 sec, 72
            degrees C for 1
            min.
            Protocol:
               Template:        50 ng
               Primer:          each 0.2 uM
               Taq Polymerase:  0.02 units/ul
               Total Vol:       50 ul

            Buffer:
               MgCl2:     2.5 mM
               KCl:       50 mM
               Tris-HCl:  10 mM
               pH:        8.3
               DMSO:      0 %.
FEATURES             Location/Qualifiers
     source          1. .266
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /sex="Male and Female"
                     /clone_lib="Random genomic STS"
     STS             1. .266
     primer_bind     1. .23
     primer_bind     complement(242. .266)
BASE COUNT       69 a     68 c     65 g     64 t
ORIGIN

  Query Match             100.0%;  Score 12;  DB 11;  Length 266;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        145 GCCTCTGGGGAG 134


RESULT 11
HSNL1243D
LOCUS       HSNL1243D               278 bp    DNA     linear   PRI 01-JUL-1996
DEFINITION  H.sapiens genomic DNA (chromosome 3; clone NL1243D).
ACCESSION   X87489
VERSION     X87489.1  GI:1418839
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 278)
  AUTHORS   Zabarovsky,E.R.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 278)
  AUTHORS   Zabarovsky,E.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-MAY-1995) Zabarovsky E.R., Microbiology and
            Tumorbiology Center, Karolinska Institute, P.O. Box 280, Stockholm,
            S-171 77, SWEDEN
FEATURES             Location/Qualifiers
     source          1. .278
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="3 (human)"
                     /clone="NL1243D"
                     /cell_line="mouse/human microcell hybrid line MHC 903.1"
                     /clone_lib="NotI linking library"
                     /note="genomic DNA surrounding NotI sites"
BASE COUNT       44 a     95 c     77 g     62 t
ORIGIN

  Query Match             100.0%;  Score 12;  DB 9;  Length 278;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        240 GCCTCTGGGGAG 251


RESULT 12
HUMCW05/c
```

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LOCUS       HUMCW05                  287 bp    DNA     linear   PRI 14-APR-2000
DEFINITION  Human DNA for HLA-Cw*0702, partial cds.
ACCESSION   D64153
VERSION     D64153.1  GI:1339908
KEYWORDS    HLA-Cw*0702; MHC class I.
SOURCE      Homo sapiens (isolate:TM) peripheral Blood lymphocyte DNA,
            clone:L-1.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Wang,H., Tokunaga,K., Ishikawa,Y., Asahina,A., Kuwata,S., Akaza,T.,
            Tadokoro,K., Shibata,Y., Takiguchi,M. and Juji,T.
  TITLE     Identification and DNA typing of two Cw7 alleles (Cw*0702 and
            Cw*0704) in Japanese, with the corrected sequence of Cw*0702
  JOURNAL   Hum. Immunol. 45 (1), 52-58 (1996)
  MEDLINE   96232973
REFERENCE   2  (bases 1 to 287)
  AUTHORS   Wang,H.
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 287)
  AUTHORS   Wang,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-SEP-1995) Huiru Wang, Japanese Red Cross Central
            Blood Center, Department of Research; 4-1-31 Hiroo, Shibuya-ku,
            Tokyo 150, Japan (Tel:03-5485-6009, Fax:03-3406-7892)
FEATURES             Location/Qualifiers
     source          1. .287
                     /organism="Homo sapiens"
                     /isolate="TM"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6p21.3"
                     /clone="L-1"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral Blood"
     exon            <1. .157
                     /number=1
     5'UTR           <1. .84
     CDS             85. .>157
                     /codon_start=1
                     /product="HLA-Cw*0702"
                     /protein_id="BAA11022.1"
                     /db_xref="GI:1561555"
                     /translation="MRVMAPRTLILLLSGALALTETWA"
     intron          158. .287
                     /number=1
BASE COUNT       45 a    101 c    103 g     38 t
ORIGIN

  Query Match             100.0%;  Score 12;  DB 9;  Length 287;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db         80 GCCTCTGGGGAG 69


RESULT 13
G09804
LOCUS       G09804                   292 bp    DNA     linear   STS 15-AUG-1995
DEFINITION  human STS CHLC.GCT13C07.P16417 clone GCT13C07, sequence tagged
            site.
ACCESSION   G09804
VERSION     G09804.1  GI:941653
KEYWORDS    STS; STS sequence; primer; sequence tagged site.
SOURCE      Homo sapiens vector=pJCP1 host=E.coli dut+ung+ (DH10B) Marker
            Selected genomic DNA prepared from XY individual of French
            nationality.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 292)
  AUTHORS   Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H.
  TITLE     Cooperative Human Linkage Center
  JOURNAL   Unpublished (1995)
COMMENT     Synonyms: GCT13C07, CHLC.GCT13C07.T16344
            Contact: Dr. Jeffrey C. Murray
            UofI
            The University of Iowa
            Department of Pediatrics, Iowa City, IA 52242, USA
            Tel: (319) 356-3508
            Fax: (319) 356-3347
            Email: jeff-murray@uiowa.edu

            Primer A: TTCTGTCACTTACTCATTGTGTAGC
            Primer B: GTTCACGTGAACAAGTTCCC
            STS size: 122
            PCR Profile:
                        denature:    30 seconds at 94 degrees C
                        annealing:   75 seconds at 55 degrees C
                        extension:   15 seconds at 72 degrees C
                        PCR cycles:  27
                        extension:    6 minutes at 72 degress C
            Protocol:
                        Template:        30ng genomic DNA
                        Primer:          each 1.5 pmole
                        dNTPs:           each 200 uM
                        Taq Polymerase:  0.3 units
                        Total Vol:       10 ul

            Buffer:
                        MgCl2:  1.5mM
                        KCl:     50mM
                        Tris:    10mM
                        pH:     8.3.
FEATURES             Location/Qualifiers
     source          1. .292
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     STS             62. .183
     primer_bind     62. .86
     primer_bind     complement(164. .183)
BASE COUNT       86 a     60 c     58 g     86 t      2 others
ORIGIN

  Query Match             100.0%;  Score 12;  DB 11;  Length 292;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        219 GCCTCTGGGGAG 230


RESULT 14
HUMUT7961A/c
LOCUS       HUMUT7961A               321 bp    DNA     linear   STS 29-DEC-1994
DEFINITION  Human STS UT7961, 5' primer bind, sequence tagged site.
ACCESSION   L30159
VERSION     L30159.1  GI:605335
KEYWORDS    STS; PCR primer; STS sequence; microsatellite DNA; microsatellite
            marker; sequence tagged site; tetranucleotide repeat.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,L.,
            Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X.,
            Robertson,M., Bradley,P., Elsner,T., Tingey,A., Lalouel,J.-M. and
            White,R.
  TITLE     Genetic and physical mapping of simple sequence repeat containing
            sequence tagged sites from the human genome
  JOURNAL   Unpublished (1994)
```

```
COMMENT     Submitted by: Utah Center for Human Genome Research University of
            Utah, Dept. of Human Genetics
            2160 Eccles Institute of Human Genetics
            Salt Lake City, UT  84112
            e-mail: sts@corona.med.utah.edu
            Primer A:  TTGGACTCCCCAGAGGCGT
            Primer B:  TTGGTCTGGGCGTGTAGTTT
            End to Label: Primer A
            PCR Profile:
            Initial Denaturation: 94C 300sec
            Cycles     Denaturation    Annealing       Extension 5          94
            C  10 sec.   54 C  10 sec.   72 C  20 sec. 30         94 C  10 sec.
              56 C  10 sec.   72 C  20 sec. Mg++: 1.00 mM
            Gel: Acrylamide 7%, Formamide 32%, Urea 34%
            Alleles: 1.
FEATURES             Location/Qualifiers
     source          1. .321
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     primer_bind     197. .215
                     /evidence=experimental
BASE COUNT       64 a    102 c     97 g     53 t      5 others
ORIGIN

  Query Match             100.0%;  Score 12;  DB 11;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 5.3e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        213 GCCTCTGGGGAG 202


RESULT 15
G71854
LOCUS       G71854                   330 bp    DNA     linear   STS 08-JUN-2001
DEFINITION  A09122834FMo17 maize leaf DNA Zea mays STS genomic, sequence tagged
            site.
ACCESSION   G71854
VERSION     G71854.1  GI:14333539
KEYWORDS    STS.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 330)
  AUTHORS   Yang,Y.J., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
  TITLE     3' UTR sequences of maize genes
  JOURNAL   Unpublished (2001)
COMMENT
            Contact: Schnable, P.S.
            Schnable laboratory
            Iowa State University
            G405 Agronomy Hall, Ames, IA 50011, USA
            Tel: 515-294-0975
            Fax: 515-294-2299
            Email: schnable@iastate.edu
            Primer A: CCTATCTATTGGGTTCTCAGC
            Primer B: GGAGAGGTCTGAATCATGG
            PCR Profile:
                 Denaturation:   94 degrees C for 30 seconds
                 Annealing:      60 degrees C for 45 seconds
                 Polymerization: 72 degrees C for 90 seconds
                 PCR cycles:     31
                 Thermal cycler: Perkin Elmer TC
            Protocol:
                   Template: 10-20 ng
                   Primer: each 0.5 uM
                   dNTPs: each 200 uM
                   Taq Polymerase: 0.05 units/ul
                   Total vol: 20 ul
            Buffer:
                  MgCl2: 2 mM
                  KCl: 50 mM
                  Tris-HCl: 20 mM
                  pH: 8.4.
FEATURES             Location/Qualifiers
     source          1. .330
                     /organism="Zea mays"
                     /strain="DE811"
                     /db_xref="taxon:4577"
                     /clone_lib="maize leaf DNA"
                     /note="PCR products amplified from genomic DNA"
     STS             <1. .>330
BASE COUNT       67 a    107 c     83 g     71 t      2 others
ORIGIN

  Query Match             100.0%;  Score 12;  DB 11;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 5.3e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db         80 GCCTCTGGGGAG 91


Search completed: June 12, 2003, 11:05:07
Job time : 987 secs
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GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 10:33:06 ; Search time 209 Seconds
(without alignments)
129.301 Million cell updates/sec

Title: US-09-761-116-1
Perfect score: 12
Sequence: 1 gcctctggggag 12

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
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12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 12 | 100.0 | 12 | 21 | AAA87902 | Human beta-3-adren |
| | 2 | 12 | 100.0 | 28 | 21 | AAA87942 | Beta-3-AR segment |
| | 3 | 12 | 100.0 | 28 | 21 | AAA87947 | Beta-3-AR segment |
| | 4 | 12 | 100.0 | 28 | 21 | AAA87948 | Beta-3-AR segment |
| | 5 | 12 | 100.0 | 28 | 21 | AAA87949 | Beta-3-AR segment |
| | 6 | 12 | 100.0 | 113 | 22 | ABA76256 | Human foetal liver |
| | 7 | 12 | 100.0 | 113 | 22 | ABA40796 | Probe #19262 for g |
| | 8 | 12 | 100.0 | 113 | 22 | AAK24907 | Human brain expres |
| | 9 | 12 | 100.0 | 113 | 22 | AAK50902 | Human bone marrow |
| | 10 | 12 | 100.0 | 113 | 22 | AAI27940 | Probe #17873 for g |
| | 11 | 12 | 100.0 | 113 | 24 | ABS24411 | Human genome-deriv |
| | 12 | 12 | 100.0 | 200 | 21 | AAA87904 | Human beta-3-adren |
| c | 13 | 12 | 100.0 | 227 | 21 | AAC15250 | Human secreted pro |
| | 14 | 12 | 100.0 | 234 | 22 | AAS30782 | Human cDNA encodin |
| | 15 | 12 | 100.0 | 289 | 24 | ABN21401 | Human ORFX polynuc |
| | 16 | 12 | 100.0 | 294 | 21 | AAC48449 | Arabidopsis thalia |
| c | 17 | 12 | 100.0 | 305 | 22 | ABA51365 | Human breast cell |
| c | 18 | 12 | 100.0 | 305 | 22 | ABA69368 | Human foetal liver |
| c | 19 | 12 | 100.0 | 305 | 22 | ABA36303 | Probe #14769 for g |
| c | 20 | 12 | 100.0 | 305 | 22 | AAK17648 | Human brain expres |
| c | 21 | 12 | 100.0 | 305 | 22 | AAK43461 | Human bone marrow |
| c | 22 | 12 | 100.0 | 305 | 22 | AAI24242 | Probe #14175 for g |
| c | 23 | 12 | 100.0 | 305 | 22 | AAI49525 | Probe #18211 used |
| c | 24 | 12 | 100.0 | 305 | 22 | AAI09803 | Probe #9794 used t |
| c | 25 | 12 | 100.0 | 305 | 24 | ABS17580 | Human genome-deriv |
| | 26 | 12 | 100.0 | 312 | 22 | AAI87082 | Human polynucleoti |
| | 27 | 12 | 100.0 | 343 | 22 | ABA07685 | Human ovarian and |
| | 28 | 12 | 100.0 | 343 | 22 | AAL02637 | Human reproductive |
| | 29 | 12 | 100.0 | 349 | 22 | ABA66473 | Human foetal liver |
| | 30 | 12 | 100.0 | 349 | 22 | ABA33535 | Probe #12001 for g |
| | 31 | 12 | 100.0 | 349 | 22 | AAK14892 | Human brain expres |
| | 32 | 12 | 100.0 | 349 | 22 | AAI46673 | Probe #15359 used |
| | 33 | 12 | 100.0 | 351 | 24 | ABL81321 | Human ovarian canc |
| | 34 | 12 | 100.0 | 360 | 21 | AAC74668 | Human ORFX ORF223 |
| c | 35 | 12 | 100.0 | 374 | 22 | AAI89863 | Human polynucleoti |
| | 36 | 12 | 100.0 | 381 | 22 | AAF67500 | Novel human polynu |
| | 37 | 12 | 100.0 | 385 | 24 | ABL82542 | Human ovarian canc |
| c | 38 | 12 | 100.0 | 402 | 21 | AAC02389 | Human secreted pro |
| | 39 | 12 | 100.0 | 403 | 24 | ABN20175 | Human ORFX polynuc |
| | 40 | 12 | 100.0 | 409 | 24 | ABK87524 | Mammalian nebulin- |
| | 41 | 12 | 100.0 | 412 | 22 | AAH98943 | Human EST-derived |
| c | 42 | 12 | 100.0 | 413 | 23 | ABV15628 | Human prostate exp |
| | 43 | 12 | 100.0 | 417 | 22 | AAI82925 | Human polynucleoti |
| | 44 | 12 | 100.0 | 435 | 22 | ABA21400 | Human nervous syst |
| c | 45 | 12 | 100.0 | 438 | 22 | ABA09485 | Human Zn metallopr |

ALIGNMENTS

RESULT 1
AAA87902
ID AAA87902 standard; DNA; 12 BP.
XX
AC AAA87902;
XX
DT 07-DEC-2000 (first entry)
XX
DE Human beta-3-adrenergic receptor B segment oligonucleotide SEQ ID NO:1.
XX
KW Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
KW regulation; identification; trans-activating factor; drug screening;
KW gene expression regulation; obesity; type II diabetes; ss.
XX
OS Homo sapiens.
XX
PN WO200044901-A1.
XX
PD 03-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US02632.
XX
PR 01-FEB-1999; 99US-0243335.
XX
PA (AMHP ) AMERICAN HOME PROD CORP.
XX
PI Susulic VS, Duzic E;
XX
DR WPI; 2000-482973/42.
XX
PT New isolated nucleic acid useful for screening assays to identify
PT compounds capable of regulating beta3-AR (adrenergic receptor)

PT expression, is composed of three regulatory segments -
XX
PS Claim 2; Page 57; 88pp; English.
XX
CC The present sequence represent the core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
XX
SQ Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCTGGGGAG 12
||||||||||||
Db 1 GCCTCTGGGGAG 12

RESULT 2
AAA87942
ID AAA87942 standard; DNA; 28 BP.
XX
AC AAA87942;
XX
DT 07-DEC-2000 (first entry)
XX
DE Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:41.
XX
KW Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
KW regulation; identification; trans-activating factor; drug screening;
KW gene expression regulation; obesity; type II diabetes; mutation; ss.
XX
OS Homo sapiens.
XX
PN WO200044901-A1.
XX
PD 03-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US02632.
XX
PR 01-FEB-1999; 99US-0243335.
XX
PA (AMHP ) AMERICAN HOME PROD CORP.
XX
PI Susulic VS, Duzic E;
XX
DR WPI; 2000-482973/42.
XX
PT New isolated nucleic acid useful for screening assays to identify
PT compounds capable of regulating beta3-AR (adrenergic receptor)
PT expression, is composed of three regulatory segments -
XX
PS Example 1; Fig 7; 88pp; English.
XX
CC The present invention describes a core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
CC The present sequence represents a human beta-3-AR segment B mutational
CC analysis oligonucleotide, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 28 BP; 4 A; 10 C; 8 G; 6 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCTGGGGAG 12
||||||||||||
Db 6 GCCTCTGGGGAG 17

RESULT 3
AAA87947
ID AAA87947 standard; DNA; 28 BP.
XX
AC AAA87947;
XX
DT 07-DEC-2000 (first entry)
XX
DE Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:46.
XX
KW Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
KW regulation; identification; trans-activating factor; drug screening;
KW gene expression regulation; obesity; type II diabetes; mutation; ss.
XX
OS Homo sapiens.
XX
PN WO200044901-A1.
XX
PD 03-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US02632.
XX
PR 01-FEB-1999; 99US-0243335.
XX
PA (AMHP ) AMERICAN HOME PROD CORP.
XX
PI Susulic VS, Duzic E;
XX
DR WPI; 2000-482973/42.
XX
PT New isolated nucleic acid useful for screening assays to identify
PT compounds capable of regulating beta3-AR (adrenergic receptor)
PT expression, is composed of three regulatory segments -
XX
PS Example 1; Fig 7; 88pp; English.
XX
CC The present invention describes a core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for
CC drug screening. It is envisaged that beta-3-AR stimulation may have
CC beneficial effects in the treatment of obesity and type II diabetes.
CC The present sequence represents a human beta-3-AR segment B mutational
CC analysis oligonucleotide, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 28 BP; 3 A; 10 C; 8 G; 7 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 28;

```
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          6 GCCTCTGGGGAG 17


RESULT 4
AAA87948
ID   AAA87948 standard; DNA; 28 BP.
XX
AC   AAA87948;
XX
DT   07-DEC-2000  (first entry)
XX
DE   Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:47.
XX
KW   Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
KW   regulation; identification; trans-activating factor; drug screening;
KW   gene expression regulation; obesity; type II diabetes; mutation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200044901-A1.
XX
PD   03-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US02632.
XX
PR   01-FEB-1999;   99US-0243335.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Susulic VS,  Duzic E;
XX
DR   WPI; 2000-482973/42.
XX
PT   New isolated nucleic acid useful for screening assays to identify
PT   compounds capable of regulating beta3-AR (adrenergic receptor)
PT   expression, is composed of three regulatory segments  -
XX
PS   Example 1; Fig 7; 88pp; English.
XX
CC   The present invention describes a core nucleotide sequence from the
CC   B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC   region. The core nucleotide sequence binds to a B-segment-binding
CC   trans-activating factor. Recombinant vectors under control of the
CC   transcription regulation region comprising nucleotide sequences
CC   containing the core nucleotide sequence from the B segment of the human
CC   beta-3-AR regulatory region provide a substrate for high throughput
CC   assays, particularly reporter gene assays to identify compounds capable
CC   of increasing or decreasing the level of expression of beta-3-AR. The
CC   nucleotide sequences can be used for regulating gene expression and for
CC   drug screening. It is envisaged that beta-3-AR stimulation may have
CC   beneficial effects in the treatment of obesity and type II diabetes.
CC   The present sequence represents a human beta-3-AR segment B mutational
CC   analysis oligonucleotide, which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 28 BP; 6 A; 9 C; 9 G; 4 T; 0 other;

  Query Match             100.0%;  Score 12;  DB 21;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          6 GCCTCTGGGGAG 17


RESULT 5
AAA87949
ID   AAA87949 standard; DNA; 28 BP.
XX
AC   AAA87949;
XX
DT   07-DEC-2000  (first entry)
XX
DE   Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:48.
XX
KW   Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
KW   regulation; identification; trans-activating factor; drug screening;
KW   gene expression regulation; obesity; type II diabetes; mutation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200044901-A1.
XX
PD   03-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US02632.
XX
PR   01-FEB-1999;   99US-0243335.
XX
PA   (AMHP ) AMERICAN HOME PROD CORP.
XX
PI   Susulic VS,  Duzic E;
XX
DR   WPI; 2000-482973/42.
XX
PT   New isolated nucleic acid useful for screening assays to identify
PT   compounds capable of regulating beta3-AR (adrenergic receptor)
PT   expression, is composed of three regulatory segments  -
XX
PS   Example 1; Fig 7; 88pp; English.
XX
CC   The present invention describes a core nucleotide sequence from the
CC   B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC   region. The core nucleotide sequence binds to a B-segment-binding
CC   trans-activating factor. Recombinant vectors under control of the
CC   transcription regulation region comprising nucleotide sequences
CC   containing the core nucleotide sequence from the B segment of the human
CC   beta-3-AR regulatory region provide a substrate for high throughput
CC   assays, particularly reporter gene assays to identify compounds capable
CC   of increasing or decreasing the level of expression of beta-3-AR. The
CC   nucleotide sequences can be used for regulating gene expression and for
CC   drug screening. It is envisaged that beta-3-AR stimulation may have
CC   beneficial effects in the treatment of obesity and type II diabetes.
CC   The present sequence represents a human beta-3-AR segment B mutational
CC   analysis oligonucleotide, which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 28 BP; 5 A; 7 C; 11 G; 5 T; 0 other;

  Query Match             100.0%;  Score 12;  DB 21;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          6 GCCTCTGGGGAG 17


RESULT 6
ABA76256
ID   ABA76256 standard; DNA; 113 BP.
XX
AC   ABA76256;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human foetal liver single exon nucleic acid probe #24561.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
```

```
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
[redacted]   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 4; SEQ ID NO 24561; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

  Query Match             100.0%;  Score 12;  DB 22;  Length 113;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db         94 GCCTCTGGGGAG 105


[redacted]LT 7
[redacted]0796
ID   ABA40796 standard; DNA; 113 BP.
XX
AC   ABA40796;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Probe #19262 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts -
XX
PS   Claim 4; SEQ ID No 19262; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart. The
CC   present sequence is one such probe. The probes may be used for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from the human heart via microarrays. By measuring gene expression, the
CC   probes are useful for predicting, diagnosing, grading, staging,
CC   monitoring and prognosing diseases of the human heart and vascular system
CC   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC   congenital heart disease.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

  Query Match             100.0%;  Score 12;  DB 22;  Length 113;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db         94 GCCTCTGGGGAG 105


RESULT 8
AAK24907
ID   AAK24907 standard; DNA; 113 BP.
XX
AC   AAK24907;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 24898.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
```

XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 24898; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

Query Match 100.0%; Score 12; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCTGGGGAG 12
||||||||||||
Db 94 GCCTCTGGGGAG 105

RESULT 9
AAK50902
ID AAK50902 standard; DNA; 113 BP.
XX
AC AAK50902;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 25459.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00668.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
PS Example 4; SEQ ID NO: 25459; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

Query Match 100.0%; Score 12; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCTGGGGAG 12
||||||||||||
Db 94 GCCTCTGGGGAG 105

RESULT 10
AAI27940
ID AAI27940 standard; DNA; 113 BP.
XX
AC AAI27940;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #17873 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 17873; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

Query Match 100.0%; Score 12; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCTGGGGAG 12
||||||||||||
Db 94 GCCTCTGGGGAG 105

RESULT 11
ABS24411
ID ABS24411 standard; DNA; 113 BP.
XX
AC ABS24411;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 24402.
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesis; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US00665.
XX
PR 04-FEB-2000; 2000US-180312P.
PR 26-MAY-2000; 2000US-207456P.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-234687P.
PR 27-SEP-2000; 2000US-236359P.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples -
XX
PS Claim 4; SEQ ID No 24402; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of
CC probes; the novel set of probes which hybridise at high stringency to a
CC nucleic acid expressed in the human lung; measuring gene expression in a
CC sample derived from human lung, comprising (a) contacting the array with
CC a collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of
CC the array; identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis,
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a single exon
CC probe open reading frame of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;

Query Match 100.0%; Score 12; DB 24; Length 113;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCTGGGGAG 12
||||||||||||
Db 94 GCCTCTGGGGAG 105

RESULT 12
AAA87904
ID AAA87904 standard; DNA; 200 BP.
XX
AC AAA87904;
XX
DT 07-DEC-2000 (first entry)
XX
DE Human beta-3-adrenergic receptor 5' flanking region SEQ ID NO:3.
XX
KW Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
KW regulation; identification; trans-activating factor; drug screening;
KW gene expression regulation; obesity; type II diabetes; ds.
XX
OS Homo sapiens.
XX
PN WO200044901-A1.
XX
PD 03-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US02632.
XX
PR 01-FEB-1999; 99US-0243335.
XX
PA (AMHP ) AMERICAN HOME PROD CORP.
XX
PI Susulic VS, Duzic E;
XX
DR WPI; 2000-482973/42.
XX
PT New isolated nucleic acid useful for screening assays to identify
PT compounds capable of regulating beta3-AR (adrenergic receptor)
PT expression, is composed of three regulatory segments -
XX
PS Claim 10; Fig 6A; 88pp; English.
XX
CC The present invention describes a core nucleotide sequence from the
CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC region. The core nucleotide sequence binds to a B-segment-binding
CC trans-activating factor. Recombinant vectors under control of the
CC transcription regulation region comprising nucleotide sequences
CC containing the core nucleotide sequence from the B segment of the human
CC beta-3-AR regulatory region provide a substrate for high throughput
CC assays, particularly reporter gene assays to identify compounds capable
CC of increasing or decreasing the level of expression of beta-3-AR. The
CC nucleotide sequences can be used for regulating gene expression and for

```
CC   drug screening. It is envisaged that beta-3-AR stimulation may have
CC   beneficial effects in the treatment of obesity and type II diabetes.
CC   The present sequence represents the human beta-3-adrenergic receptor 5'
CC   flanking region, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 200 BP; 25 A; 70 C; 37 G; 68 T; 0 other;

  Query Match             100.0%;  Score 12;  DB 21;  Length 200;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db         61 GCCTCTGGGGAG 72


RESULT 13
AAC15250/c
ID   AAC15250 standard; cDNA; 227 BP.
XX
AC   AAC15250;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 19325.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 19325; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated region (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors.
XX
SQ   Sequence 227 BP; 50 A; 53 C; 67 G; 53 T; 4 other;

  Query Match             100.0%;  Score 12;  DB 21;  Length 227;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        169 GCCTCTGGGGAG 158


RESULT 14
AAS30782
ID   AAS30782 standard; cDNA; 234 BP.
XX
AC   AAS30782;
XX
DT   04-DEC-2001  (first entry)
XX
DE   Human cDNA encoding G protein-coupled receptor nGPCR-83.
XX
KW   Human; G protein-coupled receptor; nGPCR-x; ss; antiviral; analgesic;
KW   cytostatic; cardiant; antidiabetic; anoretic; hypotensive; hypertensive;
KW   antiparkinsonian; nootropic; neuroprotective; antidepressant;
KW   viral infection; HIV-1; human immunodeficiency virus; HIV-2; pain;
KW   cancer; metabolic disease; cardiovascular disease; type 2 diabetes;
KW   obesity; anorexia; hypotension; hypertension; myocardial infarction;
KW   atherosclerosis; Parkinson's disease; psychosis; neurological disorder;
KW   schizophrenia; migraine; major depression; anxiety; mental disorder;
KW   manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200166750-A2.
XX
PD   13-SEP-2001.
XX
PF   08-MAR-2001; 2001WO-US07322.
XX
PR   08-MAR-2000; 2000US-0187581.
PR   08-MAR-2000; 2000US-0187582.
PR   08-MAR-2000; 2000US-0187714.
PR   08-MAR-2000; 2000US-0187715.
PR   08-MAR-2000; 2000US-0187825.
PR   08-MAR-2000; 2000US-0187828.
PR   08-MAR-2000; 2000US-0187829.
PR   08-MAR-2000; 2000US-0187830.
PR   08-MAR-2000; 2000US-0187833.
PR   08-MAR-2000; 2000US-0187874.
PR   08-MAR-2000; 2000US-0187930.
PR   08-MAR-2000; 2000US-0188049.
PR   08-MAR-2000; 2000US-0189294.
PR   08-MAR-2000; 2000US-0187929.
PR   08-MAR-2000; 2000US-0187928.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Vogeli G,  Wood LS;
XX
DR   WPI; 2001-536778/59.
DR   P-PSDB; AAU19213.
XX
PT   Isolated nucleic acid molecules encoding G protein-coupled receptors
PT   termed nGPCR-x, useful in the treatment and diagnosis of viral
PT   infections, cancers and mental disorders (e.g. Parkinson's disease and
PT   schizophrenia) -
XX
PS   Claim 4; Page 201; 336pp; English.
XX
CC   The invention relates to novel isolated nucleic acid molecules encoding
CC   G protein-coupled receptors termed nGPCR-x. nGPCR-x polynucleotides,
CC   polypeptides, and modulators may be used in the treatment of diseases and
CC   conditions such as infections, such as viral infections caused by HIV-1
CC   (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and
CC   cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity,
CC   anorexia, hypotension, hypertension, myocardial infarction,
CC   atherosclerosis), Parkinson's disease, and psychotic and
CC   neurological disorders, including schizophrenia, migraine, major
CC   depression, anxiety, mental disorder, manic depression, and
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CC   dyskinesias, such as Huntington's disease or Tourette's Syndrome
CC   and many other diseases and syndromes listed in the specification.
CC   nGPCR-x polynucleotides and polypeptides, as well as nGPCR-x
CC   modulators, may also be used in diagnostic assays for such diseases or
CC   conditions. The present sequence encodes a G protein-coupled
CC   receptor of the invention.
XX
SQ   Sequence 234 BP; 56 A; 64 C; 65 G; 49 T; 0 other;

  Query Match             100.0%;  Score 12;  DB 22;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        100 GCCTCTGGGGAG 111


RESULT 15
AB[redacted]21401
[redacted] ABN21401 standard; cDNA; 289 BP.
XX
AC   ABN21401;
XX
DT   24-JUN-2002  (first entry)
XX
DE   Human ORFX polynucleotide sequence SEQ ID NO:11279.
XX
KW   Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW   hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW   degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW   cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW   hypertension; hypothyroidism; cholesterol ester storage disease;
KW   immune deficiency; immune disorder; infectious disease;
KW   autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW   myasthenia gravis; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192523-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US10836.
XX
PR   30-MAY-2000; 2000US-206132P.
PR   29-AUG-2000; 2000US-228716P.
XX
[redacted] (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach MD;
XX
DR   WPI; 2002-106308/14.
DR   P-PSDB; ABP05649.
XX
PT   Novel human polypeptides and polynucleotides useful for diagnosing,
PT   preventing and treating cardiovascular disease, neurodegenerative,
PT   hyperproliferative disorders and autoimmune disorders -
XX
PS   Disclosure; SEQ ID 11279; 1037pp; English.
XX
CC   The present invention describes substantially purified human proteins
CC   (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC   in the specification). ABN15762 to ABN27252 encode the human ORFX
CC   proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC   treating or preventing a pathology associated with an ORFX-associated
CC   disorder in humans, and in the manufacture of a medicament for treating a
CC   syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC   sequences can be used in gene therapy. ORFX sequences can be used in the
CC   treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC   psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC   osteoarthritis, neurodegenerative disorders, disorders related to organ
CC   transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC   lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC   storage disease, various immune deficiencies and disorders, infectious
CC   diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC   arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC   disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC   useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC   bone degenerative disorders, or periodontal disease, and for gut
CC   protection or regeneration and treatment of lung or liver fibrosis,
CC   reperfusion injury in various tissues and conditions resulting from
CC   systemic cytokine damage.
CC   N.B.  The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 289 BP; 45 A; 75 C; 117 G; 52 T; 0 other;

  Query Match             100.0%;  Score 12;  DB 24;  Length 289;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db         31 GCCTCTGGGGAG 42


Search completed: June 12, 2003, 10:48:27
Job time : 210 secs
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GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 10:39:36 ; Search time 64 Seconds
(without alignments)
57.502 Million cell updates/sec

Title: US-09-761-116-1
Perfect score: 12
Sequence: 1 gcctctggggag 12

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 12 | 100.0 | 12 | 4 | US-09-243-335-1 | Sequence 1, Appli |
| | 2 | 12 | 100.0 | 28 | 4 | US-09-243-335-41 | Sequence 41, Appl |
| | 3 | 12 | 100.0 | 28 | 4 | US-09-243-335-46 | Sequence 46, Appl |
| | 4 | 12 | 100.0 | 28 | 4 | US-09-243-335-47 | Sequence 47, Appl |
| | 5 | 12 | 100.0 | 28 | 4 | US-09-243-335-48 | Sequence 48, Appl |
| | 6 | 12 | 100.0 | 200 | 4 | US-09-243-335-3 | Sequence 3, Appli |
| c | 7 | 12 | 100.0 | 1279 | 1 | US-08-146-010A-4 | Sequence 4, Appli |
| c | 8 | 12 | 100.0 | 1279 | 1 | US-08-674-168-9 | Sequence 9, Appli |
| c | 9 | 12 | 100.0 | 1363 | 1 | US-08-776-088-21 | Sequence 21, Appl |
| c | 10 | 12 | 100.0 | 1363 | 5 | PCT-US95-09145A-21 | Sequence 21, Appl |
| c | 11 | 12 | 100.0 | 1820 | 4 | US-09-732-199A-3 | Sequence 3, Appli |
| c | 12 | 12 | 100.0 | 1868 | 4 | US-09-739-455-1 | Sequence 1, Appli |
| c | 13 | 12 | 100.0 | 1875 | 3 | US-08-878-474-4 | Sequence 4, Appli |
| c | 14 | 12 | 100.0 | 1878 | 4 | US-09-732-025-1 | Sequence 1, Appli |
| | 15 | 12 | 100.0 | 1938 | 1 | US-08-278-635B-1 | Sequence 1, Appli |
| | 16 | 12 | 100.0 | 1938 | 3 | US-08-464-258B-1 | Sequence 1, Appli |
| | 17 | 12 | 100.0 | 1938 | 3 | US-08-471-961-1 | Sequence 1, Appli |
| | 18 | 12 | 100.0 | 2109 | 4 | US-09-370-838-153 | Sequence 153, App |
| | 19 | 12 | 100.0 | 2363 | 4 | US-08-487-596-5 | Sequence 5, Appli |
| | 20 | 12 | 100.0 | 2374 | 2 | US-08-466-589-5 | Sequence 5, Appli |
| | 21 | 12 | 100.0 | 2374 | 2 | US-08-700-636-5 | Sequence 5, Appli |
| | 22 | 12 | 100.0 | 2374 | 3 | US-08-467-574-5 | Sequence 5, Appli |
| | 23 | 12 | 100.0 | 2374 | 4 | US-09-217-345-5 | Sequence 5, Appli |
| c | 24 | 12 | 100.0 | 2540 | 1 | US-08-446-919A-1 | Sequence 1, Appli |
| | 25 | 12 | 100.0 | 2577 | 2 | US-08-209-521-25 | Sequence 25, Appl |
| c | 26 | 12 | 100.0 | 2655 | 4 | US-08-456-200B-10 | Sequence 10, Appl |
| c | 27 | 12 | 100.0 | 4837 | 4 | US-09-629-616-1 | Sequence 1, Appli |
| c | 28 | 12 | 100.0 | 5176 | 4 | US-09-182-024A-1 | Sequence 1, Appli |
| c | 29 | 12 | 100.0 | 5434 | 2 | US-08-841-349-1 | Sequence 1, Appli |
| c | 30 | 12 | 100.0 | 7032 | 2 | US-08-149-097D-24 | Sequence 24, Appl |
| c | 31 | 12 | 100.0 | 7032 | 3 | US-08-949-386-24 | Sequence 24, Appl |
| c | 32 | 12 | 100.0 | 7032 | 3 | US-08-450-562-24 | Sequence 24, Appl |
| c | 33 | 12 | 100.0 | 7032 | 4 | US-08-984-709A-24 | Sequence 24, Appl |
| c | 34 | 12 | 100.0 | 7032 | 4 | US-08-450-272-24 | Sequence 24, Appl |
| c | 35 | 12 | 100.0 | 7089 | 3 | US-08-949-386-25 | Sequence 25, Appl |
| c | 36 | 12 | 100.0 | 7089 | 3 | US-08-450-562-25 | Sequence 25, Appl |
| c | 37 | 12 | 100.0 | 7089 | 4 | US-08-984-709A-25 | Sequence 25, Appl |
| c | 38 | 12 | 100.0 | 7089 | 4 | US-08-450-272-25 | Sequence 25, Appl |
| c | 39 | 12 | 100.0 | 8285 | 4 | US-09-732-025-3 | Sequence 3, Appli |
| | 40 | 12 | 100.0 | 8310 | 3 | US-08-870-126-11 | Sequence 11, Appl |
| | 41 | 12 | 100.0 | 8310 | 4 | US-09-445-247-11 | Sequence 11, Appl |
| c | 42 | 12 | 100.0 | 11827 | 4 | US-09-739-455-3 | Sequence 3, Appli |
| | 43 | 12 | 100.0 | 14985 | 1 | US-08-652-972A-6 | Sequence 6, Appli |
| | 44 | 12 | 100.0 | 14985 | 5 | PCT-US96-06231A-6 | Sequence 6, Appli |
| | 45 | 12 | 100.0 | 16389 | 4 | US-09-741-154-3 | Sequence 3, Appli |

ALIGNMENTS

RESULT 1
US-09-243-335-1
; Sequence 1, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; APPLICANT: Duzic, Edmir
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE
; FILE REFERENCE: 0630/0E791
; CURRENT APPLICATION NUMBER: US/09/243,335A
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-243-335-1

Query Match 100.0%; Score 12; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCCTCTGGGGAG 12
||||||||||||
Db 1 GCCTCTGGGGAG 12

RESULT 2
US-09-243-335-41
; Sequence 41, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; APPLICANT: Duzic, Edmir
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE
; FILE REFERENCE: 0630/0E791
; CURRENT APPLICATION NUMBER: US/09/243,335A
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 28
; TYPE: DNA

```
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-243-335-41

  Query Match             100.0%;  Score 12;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          6 GCCTCTGGGGAG 17


RESULT 3
US-09-243-335-46
; Sequence 46, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
;  APPLICANT: American Home Products Corp.
;  APPLICANT: Susulic, Vedrana S.
;  APPLICANT: Duzic, Edmir
;  TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
;  TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE
;  FILE REFERENCE: 0630/0E791
;  CURRENT APPLICATION NUMBER: US/09/243,335A
;  CURRENT FILING DATE: 1999-02-01
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 46
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-243-335-46

  Query Match             100.0%;  Score 12;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          6 GCCTCTGGGGAG 17


RESULT 4
US-09-243-335-47
; Sequence 47, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
;  APPLICANT: American Home Products Corp.
;  APPLICANT: Susulic, Vedrana S.
;  APPLICANT: Duzic, Edmir
;  TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
;  TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE
;  FILE REFERENCE: 0630/0E791
;  CURRENT APPLICATION NUMBER: US/09/243,335A
;  CURRENT FILING DATE: 1999-02-01
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 47
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-243-335-47

  Query Match             100.0%;  Score 12;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          6 GCCTCTGGGGAG 17


RESULT 5
US-09-243-335-48
; Sequence 48, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
;  APPLICANT: American Home Products Corp.
;  APPLICANT: Susulic, Vedrana S.
;  APPLICANT: Duzic, Edmir
;  TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
;  TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE
;  FILE REFERENCE: 0630/0E791
;  CURRENT APPLICATION NUMBER: US/09/243,335A
;  CURRENT FILING DATE: 1999-02-01
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 48
;   LENGTH: 28
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-243-335-48

  Query Match             100.0%;  Score 12;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db          6 GCCTCTGGGGAG 17


RESULT 6
US-09-243-335-3
; Sequence 3, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
;  APPLICANT: American Home Products Corp.
;  APPLICANT: Susulic, Vedrana S.
;  APPLICANT: Duzic, Edmir
;  TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
;  TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE
;  FILE REFERENCE: 0630/0E791
;  CURRENT APPLICATION NUMBER: US/09/243,335A
;  CURRENT FILING DATE: 1999-02-01
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 200
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
US-09-243-335-3

  Query Match             100.0%;  Score 12;  DB 4;  Length 200;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db         61 GCCTCTGGGGAG 72


RESULT 7
US-08-146-010A-4/c
; Sequence 4, Application US/08146010A
; Patent No. 5591577
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  TSUCHIYA, MAKOTO
;    APPLICANT:  MORIYA, MIKO
;    APPLICANT:  MIWA, KIYOSHI
;    TITLE OF INVENTION:  MOBILE GENETIC ELEMENT ORIGINATED FROM
;    TITLE OF INVENTION:  BREVIBACTERIUM STRAIN
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,010A
;      FILING DATE:  12-NOV-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 52694/92
;      FILING DATE:  11-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  10-649-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1279 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Brevibacterium lactofermentum
;      STRAIN:  AJ2256
;    FEATURE:
;      NAME/KEY:  insertion_seq
;      LOCATION:  1..1279
US-08-146-010A-4

  Query Match            100.0%;  Score 12;  DB 1;  Length 1279;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        136 GCCTCTGGGGAG 125


RESULT 8
US-08-674-168-9/c
; Sequence 9, Application US/08674168
; Patent No. 5804414
;  GENERAL INFORMATION:
;    APPLICANT:  MORIYA, Mika
;    APPLICANT:  MATSUI, Hiroshi
;    APPLICANT:  YOKOZEKI, Kenzo
;    APPLICANT:  HIRANO, Seiko
;    APPLICANT:  HAYAKAWA, Atsushi
;    APPLICANT:  IZUI, Masako
;    APPLICANT:  SUGIMOTO, Masakazu
;    TITLE OF INVENTION:  METHOD OF AMPLIFYING GENE USING
;    TITLE OF INVENTION:  ARTIFICIAL TRANSPOSON
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/674,168
;      FILING DATE:  01-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-166541
;      FILING DATE:  30-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  10-810-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1279 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Brevibacterium lactofermentum
;      STRAIN:  AJ12036
;    FEATURE:
;      NAME/KEY:  repeat_region
;      LOCATION:  1..14
;    FEATURE:
;      NAME/KEY:  repeat_region
;      LOCATION:  1266..1279
US-08-674-168-9

  Query Match            100.0%;  Score 12;  DB 1;  Length 1279;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        136 GCCTCTGGGGAG 125


RESULT 9
US-08-776-088-21/c
; Sequence 21, Application US/08776088
; Patent No. 5773579
;  GENERAL INFORMATION:
;    APPLICANT:  Torczynski, Richard M.
;    APPLICANT:  Bollon, Arthur P.
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SIDLEY & AUSTIN
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/776,088
;      FILING DATE:  19-JUL-95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Eugenia S. Hansen
;      REGISTRATION NUMBER:  31,966
;      REFERENCE/DOCKET NUMBER:  10365/05011
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-981-3300
;      TELEFAX:  214-981-3400
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1363 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-776-088-21

  Query Match             100.0%;  Score 12;  DB 1;  Length 1363;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        183 GCCTCTGGGGAG 172


RESULT 10
PCT-US95-09145A-21/c
; Sequence 21, Application PC/TUS9509145A
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Lung Cancer Marker
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RICHARDS, MEDLOCK & ANDREWS
;      STREET:  1201 Elm Street, Suite 4500
;      CITY:  Dallas
;      STATE:  TX
;      COUNTRY:  US
;      ZIP:  75270-2197
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/09145A
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  John A. Harre
;      REGISTRATION NUMBER:  37,345
;      REFERENCE/DOCKET NUMBER:  B35792CIPPCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  214-939-4500
;      TELEFAX:  214-939-4600
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1363 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US95-09145A-21

  Query Match             100.0%;  Score 12;  DB 5;  Length 1363;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        183 GCCTCTGGGGAG 172


RESULT 11
US-09-732-199A-3/c
; Sequence 3, Application US/09732199A
; Patent No. 6379960
; GENERAL INFORMATION:
;  APPLICANT: Ian Popoff
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 2, P48
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0214
;  CURRENT APPLICATION NUMBER: US/09/732,199A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 57
; SEQ ID NO 3
;   LENGTH: 1820
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (176)...(1459)
US-09-732-199A-3

  Query Match             100.0%;  Score 12;  DB 4;  Length 1820;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        113 GCCTCTGGGGAG 102


RESULT 12
US-09-739-455-1/c
; Sequence 1, Application US/09739455
; Patent No. 6413756
; GENERAL INFORMATION:
;  APPLICANT: YAN, Chunhua et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000653
;  CURRENT APPLICATION NUMBER: US/09/739,455
;  CURRENT FILING DATE:  2000-12-19
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1868
;   TYPE: DNA
;   ORGANISM: Human
US-09-739-455-1

  Query Match             100.0%;  Score 12;  DB 4;  Length 1868;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        794 GCCTCTGGGGAG 783


RESULT 13
US-08-878-474-4/c
; Sequence 4, Application US/08878474
; Patent No. 6133232
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  De Robertis, Edward M.
;    APPLICANT:  Bouwmeester, Tewis
;    TITLE OF INVENTION:  Endoderm, Cardiac and Neural Inducing
;    TITLE OF INVENTION:  Factors
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Majestic, Parsons, Siebert & Hsue
;      STREET:  Four Embarcadero Center, Suite 1100
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  94111-4106
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/878,474
;      FILING DATE:  18-JUN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/020,150
;      FILING DATE:  20-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Siebert, J. Suzanne
;      REGISTRATION NUMBER:  28,758
;      REFERENCE/DOCKET NUMBER:  3100.002US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/248-5500
;      TELEFAX:  415/362-5418
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1875 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-878-474-4

  Query Match           100.0%;  Score 12;  DB 3;  Length 1875;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        769 GCCTCTGGGGAG 758


RESULT 14
US-09-732-025-1/c
; Sequence 1, Application US/09732025
; Patent No. 6416990
; GENERAL INFORMATION:
;  APPLICANT: WEI, Ming-Hui et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001011
;  CURRENT APPLICATION NUMBER: US/09/732,025
;  CURRENT FILING DATE:  2000-12-07
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1878
;   TYPE: DNA
;   ORGANISM: Human
US-09-732-025-1

  Query Match           100.0%;  Score 12;  DB 4;  Length 1878;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        808 GCCTCTGGGGAG 797


RESULT 15
US-08-278-635B-1
; Sequence 1, Application US/08278635B
; Patent No. 5683912
;  GENERAL INFORMATION:
;    APPLICANT:  ELGOYHEN, ANA BELEN
;    APPLICANT:  JOHNSON, DAVID S.
;    APPLICANT:  BOULTER, JAMES R.
;    APPLICANT:  HEINEMANN, STEPHEN F.
;    TITLE OF INVENTION:  CLONING AND EXPRESSION OF A NOVEL
;    TITLE OF INVENTION:  ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GRAY CARY WARE & FREIDENRICH
;      STREET:  4365 EXECUTIVE DRIVE, SUITE 1600
;      CITY:  SAN DIEGO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/278,635B
;      FILING DATE:  21-JUL-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  REITER, STEPHEN E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P41 9771
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-677-1409
;      TELEFAX:  619-677-1465
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1938 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    IMMEDIATE SOURCE:
;      CLONE:  ALPHA 9
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  89..1525
US-08-278-635B-1

  Query Match           100.0%;  Score 12;  DB 1;  Length 1938;
  Best Local Similarity  100.0%;  Pred. No. 2.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCCTCTGGGGAG 12
              ||||||||||||
Db        878 GCCTCTGGGGAG 889


Search completed: June 12, 2003, 11:30:37
Job time : 65 secs
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